ı,

```
synw(deactivating,n).
synw(deactivating, ving).
synw(deactivation,n).
synw(death,n).
synw(demethylate, v).
synw(demethylate, vp).
synw(demethylated, ved).
synw(demethylated, ven).
synw(demethylates, vp).
synw(demethylating,n).
synw(demethylating, ving).
synw(demethylation, n).
synw(dephosphorylate, v).
synw(dephosphorylate, vp).
synw(dephosphorylated, ved).
synw(dephosphorylated, ven).
synw(dephosphorylates, vp).
synw(dephosphorylating, n).
synw(dephosphorylating, ving).
synw(dephosphorylation, n).
synw(die,v).
synw(die,vp).
synw(died, ved).
synw(died, ven).
synw(dies, vp).
synw(disassemble, v).
synw(disassemble, vp).
synw(disassembled, ved).
synw(disassembled, ven).
synw(disassembles, vp).
synw(disassembling, n).
synw(disassembling, ving).
synw(disassembly, n).
synw(discharge, n).
synw(discharge, v).
synw(discharge, vp).
synw(discharged, ved):
synw(discharged, ven).
synw(discharges, vp).
synw(discharging,n).
synw(discharging, ving).
synw(disengage, v).
synw(disengage, vp).
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synw(constrain, vp).
synw(constrained, ved).
synw(constrained, ven).
synw(constraining,n).
synw(constraining, ving).
synw(constrains, vp).
synw(constraint,n).
synw(coprecipitate, v).
synw(coprecipitate, vp).
synw(coprecipitated, ved).
synw(coprecipitated, ven).
synw(coprecipitates, vp).
synw(coprecipitating,n).
synw(coprecipitating, ving).
synw(coprecipitation ,n).
synw(copurification ,n).
synw(copurified , ved).
synw(copurified ,ven).
synw(copurifies, vp).
synw(copurify, vp).
synw(copurify,v).
synw(copurifying ,n).
synw(copurifying , ving).
synw(couple , vp).
synw(couple, v).
synw(coupled, ved).
synw(coupled, ven).
synw(couples, vp).
synw(coupling,n).
synw(coupling, ving).
synw(cut,n).
synw(cut,v).
synw(cut, ved).
synw(cut, ven).
synw(cut, vp).
synw(cuts, vp).
synw(cutting,n).
synw(cutting, ving).
synw(deactivate, v).
synw(deactivate, vp).
synw(deactivated, ved).
synw(deactivated, ven).
synw(deactivates, vp).
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synw(causing, n).
synw(causing, ving).
synw(cleavage,n).
synw(cleave, v).
synw(cleave, vp).
synw(cleaved, ved).
synw(cleaved, ven).
synw(cleaves, vp).
synw(cleaving,n).
synw(cleaving, ving).
synw(coimmunoprecipitate , v).
synw(coimmunoprecipitate, vp).
synw(coimmunoprecipitated, ved).
synw(coimmunoprecipitated, ven).
synw(coimmunoprecipitates, vp).
synw(coimmunoprecipitating ,n).
synw(coimmunoprecipitating , ving).
synw(coimmunoprecipitation ,n).
synw(combination ,n).
synw(combine ,v).
synw(combine , vp).
synw(combined , ved).
synw(combined , ven).
synw(combines, vp).
synw(combining ,n).
synw(combining , ving).
synw(conjugate ,v).
synw(conjugate , vp).
synw(conjugated , ve).
synw(conjugated , ved) .
synw(conjugates, vp).
synw(conjugating ,n).
synw(conjugating , ving).
synw(conjugation ,n).
synw(connect , vp).
synw(connect, v).
synw(connected , ve) . -
synw(connected , ved).
synw(connecting ,n).
synw(connecting , ving).
synw(connection ,n).
synw(connects,vp).
synw(constrain, v).
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synw(attached , ven).
synw(attaches, vp).
synw(attaching ,n).
synw(attaching , ving).
synw(attachment,n).
synw(bind,v).
synw(bind, vp).
synw(binding,h).
synw(binding, ving).
synw(binds, vp).
synw(block, v).
synw(block, vp).
synw(blockage,n).
synw(blocked, ved).
synw(blocked, ven).
synw(blocking,n).
synw(blocking, ving).
synw(blocks, vp).
synw(bound, ved).
synw(bound, ven).
synw(break, v).
synw(break, vp).
synw(breakage, n).
synw(breaking,n).
synw(breaking,ving).
synw(breaks, vp).
synw(broke, ved).
synw(broken, ven).
synw(catalyzation,n).
synw(catalyze,v).
synw(catalyze, vp).
synw(catalyzed, ved).
synw(catalyzed, ven).
synw(catalyzes,vp).
synw(catalyzing,n).
synw(catalyzing, ving).
synw(causation,n).
synw(cause, n).
synw(cause, v).
synw(cause, ven).
synw(cause, vp).
synw(caused, ved).
synw(causes, vp).
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```
synw(activate, vp).
synw(activated, ved).
synw(activated, ven).
synw(activates, vp).
synw(activating,n).
synw(activating, ving).
synw(activation, n).
synw(add, v).
synw(add, vp).
synw(added, ved).
synw(added, ven).
synw(adding,n).
synw(adding, ving).
synw(addition, n).
synw(adds, vp).
synw(after, prep).
synw(aggregate , v).
synw(aggregate , vp).
synw(aggregated , ved).
synw(aggregated , ven).
synw(aggregates, vp).
synw(aggregating ,n).
synw(aggregating , ving).
synw(aggregation ,n).
synw(arrest, n).
synw(arrest, v).
synw(arrest, vp).
synw(arrested, ved).
synw(arrested, ven).
synw(arresting,n).
synw(arresting, ving).
synw(arrests, vp).
synw(associate, v).
synw(associate, vp).
synw(associated, ved).
synw(associated, ven).
synw(associates, vp).
synw(associating,n).
synw(associating, ving).
synw(association,n).
synw(attach ,v).
synw(attach, vp).
synw(attached , ved).
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symp(set, [set, free], vp).
synp(sets, [sets, free], vp).
synp(sets, [sets, free], vp).
synp(setting, [setting, free],n).
symp(setting, [setting, free],n).
synp(setting, [setting, free], ving).
symp(setting, [setting, free], ving).
synp(suppress, [suppress, activity, of], v).
synp(suppress, [suppress, activity, of], vp).
symp(suppressed, [suppressed, activity, of], ved).
synp(suppressed, [suppressed, activity, of], ven).
synp(suppresses, [suppresses, activity, of], vp).
synp(suppressing, [suppressing, activity, of],n).
symp(suppressing, [suppressing, activity, of], ving).
symp(suppression, [suppression, of, activity, of], n).
synp(switch,[switch, on, the, activity, of], vp).
synp(switched,[switched, on, the, activity, of], ved).
synp(switched, [switched, on, the, activity, of], ved).
synp(switched,[switched, on, the, activity, of], ved).
synp(switched, [switched, on, the, activity, of], ved).
synp(switched, [switched, on, the, activity, of], ved).
synp(switches, [switches, on, the, activity, of], vp).
synp(up,[up,'-',regulate],v). % A up-regulates B B --> A
synp(up,[up,'-',regulate],vp). % A up-regulates B B --> A
synp(up, [up, '-', regulated], ved).
synp(up, [up, '-', regulated], ven). % A up-regulates B B --> A
synp(up, [up, '-', regulates], vp).
synp(up,[up,'-',regulating],n). % A up-regulates B B --> A
synp(up, [up, '-', regulating], ving). % A up-regulates B B --> A
symp(up, [up, '-', regulation], n).
synp(was, [was,a,means,of, producing], ved).
synp(was, [was,due,to],ved).
synp(were, [were,a,means,of, producing],ved). % ?
synp(were, [were,due,to],ved).
synw(acetylate, v).
synw(acetylate, vp).
synw(acetylated, ved).
synw(acetylated, ven).
synw(acetylates, vp).
synw(acetylating,n).
synw(acetylating, ving).
synw(acetylation,n).
synw(activate, v).
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synp(n,[n,'-',glycosylates],vp).
synp(n, [n, '-', glycosylating], n).
synp(n,[n,'-',glycosylating],ving).
synp(n, [n,'-',glycosylation],n).
synp(n, [n, '-', terminal, proteolysis], n).
synp(o,[o,'-',glycosylate],v).
symp(o, [o, '-', qlycosylate], vp).
synp(o,[o,'-',glycosylated],ved).
synp(o,[o,'-',glycosylated],ven).
synp(o,[o,'-',glycosylates],vp).
symp(o,[o,'-',glycosylating],n).
synp(o,[o,'-',glycosylating],ving).
symp(o, [o, '-', glycosylation], n).
synp(only, [only, after], prep).
synp(prolyl, [prolyl,'-',4,'-',hydroxylate],v ).
synp(prolyl, [prolyl,'-',4,'-',hydroxylate],vp).
synp(prolyl, [prolyl,'-',4,'-',hydroxylated],ved ).
synp(prolyl, [prolyl,'-',4,'-',hydroxylated],ven ).
synn(prolyl, [prolyl,'-',4,'-',hydroxylates],vp).
synp(prolyl, [prolyl,'-',4,'-',hydroxylating],n).
synp(prolyl, [prolyl,'-',4,'-',hydroxylating],ving ).
synp(prolyl, [prolyl,'-',4,'-',hydroxylation],n).
synp(result, [result, from], v).
symp(result, [result, from], vp).
symp(result, [result, in], v).
synp(result, [result, in], vp).
symp(resulted, [resulted, from], ved).
synp(resulted, [resulted, from], ven).
symp(resulted, [resulted, in], ved).
symp(resulted, [resulted, in], ven).
symp(resulting, [resulting, from], n).
synp(resulting, [resulting, from], ving).
symp(resulting, [resulting,in],n).
symp(resulting,[resulting,in],ving).
symp(results, [results, from], vp).
synp(results,[results,in],vp).
symp(set, [set, free], v).
symp(set, [set, free], v).
symp(set, [set, free], ved).
symp(set, [set, free], ved).
symp(set, [set, free], ven).
symp(set, [set, free], ven).
symp(set, [set, free], vp).
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synp(having, [having, an, active, role, in], n).
synp(having, [having, an, active, role, in], ving).
synp(is, [is,a,means,of, producing],vp).
symp(is, [is,due,to],vp).
synp(functions, [functions, as, a, negative, regulator, of], vp).
synp(function, [function, as, a, negative, regulator, of], vp).
synp(lead, [lead,to],v).
symp(leads, [leads,to],vp).
symp(leading, [leading, to], n).
symp(leading, [leading, to], ving ).
symp(leads, [leads,to],vp).
symp(led, [led, to], ved).
symp(led, [led, to], ven).
synp(may, [may, be, responsible, for], vp).
synp(mediate, [mediate, a, signal], v).
                                             %A mediates a signal to
synp(mediate,[mediate, a, signal], vp).
synp(mediated, [mediated, a, signal], ved).
synp(mediated, [mediated, a, signal], ven).
symp(mediates, [mediates, a, signal], vp).
synp (mediating, [mediating, a, signal], n).
synp (mediating, [mediating, a, signal], ving).
synp(mediation, [mediation, of, a, signal], n).
synp(n,[n,'-',acetylate],v).
synp(n,[n,'-',acetylate],vp).
synp(n, [n, '-', acetylated], ved).
synp(n,[n,'-',acetylated],ven).
synp(n, [n, '-', acetylates], vp).
synp(n,[n,'-',acetylating],n).
synp(n,[n,'-',acetylating],ving).
symp(n, [n, '-', acetylation], n).
symp(n, [n, '-', acylate], v).
symp(n, [n, '-', acylate], vp).
symp(n, [n, '-', acylated], ved).
synp(n,[n,'-',acylated],ven).
synp(n,[n,'-',acylates],vp).
synp(n,[n,'-',acylating],n).
synp(n,[n,'-',acylating],ving).
synp(n,[n,'-',acylation],n).
synp(n, [n, '-', glycosylate], v).
synp(n, [n, '-', glycosylate], vp).
synp(n, [n, '-', glycosylated], ved).
synp(n,[n,'-',glycosylated],ven).
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```
symp(being, [being, due, to], n).
synp(being, [being, due, to], ving).
synp(caused, [caused,by],ved).
synp(caused, [caused, by], ven).
symp(convey, [convey, a, signal], v).
symp(convey, [convey, a, signal], vp):
synp(conveyed, [conveyed, a, signal], ved).
synp(conveyed,[conveyed,a, signal],ven).
synp(conveying,[conveying, a, signal], ving).
symp(conveying,[conveying,a, signal],n).
synp(conveys, [conveys, a, signal], vp).
symp(dissociate, [dissociate, from], vp).
synp (dissociate, [dissociate, from], v).
synp(dissociated,[dissociated,from],ved).
synp (dissociated, [dissociated, from], ven).
symp(dissociates, [dissociates, from], vp).
symp (dissociating, [dissociating, from], n).
synp (dissociating, [dissociating, from], ving).
symp(dissociation, [dissociation, from], n).
synp(down, [down, '-', regulate], v).
Α
synp(down, [down, '-', regulated], ved).
synp(down, [down, '-', regulated], ven).
symp(down, [down, '-', regulates], vp).
synp(down, [down, '-', regulating], n).
synp(down, [down, '-', regulating], ving).
synp(down, [down, '-', regulation], n).
symp(due, [due, to, the, fact, that], adj).
synp(due,[due,to],adi). % ?
symp(form, [form, complex], v).
symp(form, [form, complex], vp).
symp(formation, [formation, of, complex], n).
symp(formed, [formed, complex], ved).
symp(formed, [formed, complex], ven).
symp(forming,[forming, complex],n).
symp(forming, [forming, complex], ving).
symp(forms, [forms, complex], vp).
synp(had, [had, an, active, role, in], ved).
symp(had, [had, an, active, role, in], ven).
symp(has, [has,an,active,role,in],vp).
symp(have, [have, an, active, role, in], v).
symp(have, [have, an, active, role, in], vp).
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```
% lexsyn.pat
% revised March 17, 2000
                 SYNTACTIC LEXICON FOR ACTIONS
% Contains syntactic entries for action type words and phrases
% synp(+Word1,+Wordlist,+Syn)
% synp: Wordl is first word of phrase, Wordlist is list of words i
n phrase
% synp: Syn is syntactic categorey
% synw(+Word,+Syn) is same as synp except there is no wordlist
synp(account,[account,for],v).
synp(account, [account, for], vp).
symp(accounted, [accounted, for], ved).
symp(accounted, [accounted, for], ven).
symp(accounting, [accounting, for], ving).
symp(accounting, [accounting, for], n).
synp(accounts, [accounts, for], vp).
symp(add, [add, up], vp).
symp(add, [add, up], v).
synp(added, [added, up], ved).
symp(added, [added, up], ven).
synp(adding, [adding, up], n).
synp(adding, [adding, up], ving).
synp(adds, [adds, up], vp).
synp(am, [am,a,means,of, producing],vp).
synp(am, [am, due, to], vp).
synp(are, [are,a,means,of, producing],vp).
synp(are, [are, due, to], vp).
synp(as, [as,a,result,of],prep).
synp(attributable, [attributable, to], vp). % ?
synp(attributed,[attributed,to],ven).
synp(based, [based, on], ven).
synp (based, [based, upon], ven).
synp(be, [be,a,means,of, producing],v).
symp(be, [be,due,to],v).
synp(because,[because,of],prep).
synp(been, [been, a, means, of, producing], ven).
synp(been, [been,due,to],ven).
synp(being, [being,a,means,of, producing],n).
synp(being, [being, a, means, of, producing], ving).
```

Appendix B Page 1

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wdef(pkc,protein, 'protein kinase C').
wdef(position, site, site).
wdef(positions, site, site).
wdef (protease, protein, protease).
wdef(ps1,protein,'presenilin 1').
wdef(ps2,protein,'presenilin 2').
wdef(rap1, protein, 'Rap1').
wdef(ras, protein, 'Ras').
wdef(receptors, substance, receptor).
wdef(rela, protein, 'RelA').
wdef (residues, substance, residue).
wdef(responsive, state, active).
wdef(s6, protein, 'S6').
wdef(selectively, constraint, selective).
wdef(ser112, site, 'Ser112').
wdef(ser136, site, 'Ser136').
wdef(ser32, smallmolecule, 'Ser32').
phrase(ps1, protein
wdef(ser36, smallmolecule, 'Ser36').
phrase(ps1, protein, [ps1,'-',ctf], 'ps1-ctf',r).
wdef(sh2,domain, 'SH2').
wdef(sh3,domain,'SH3').
wdef(shc, protein, 'Shc').
wdef(signalsome, complex, signalsome).
wdef(sites, site, site).
wdef(sos, protein, 'Sos').
wdef(staurosporine, smallmolecule, staurosporine).
wdef(sts, smallmolecule, 'STS').
wdef(tcr, complex, 'T-cell receptor').
wdef(tetracycline, smallmolecule,tetracycline).
wdef(thr229, aminoacid, 'Thr229').
wdef(thr308, aminoacid, 'Thr308').
wdef(thr389, aminoacid, 'Thr389').
wdef(threonine, aminoacid, threonine).
wdef(tyrosine, aminoacid, tyrosine).
wdef (unresponsive, state, inactive).
wdef(unstimulated, state, inactive).
wdef(zvad, smallmolecule, 'zVAD').
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-112	- 97		-112	-97		-112	-97		-112	-97		-112	-97		-112	- 97		-112	- 97		-112	- 97		-112	-97		-112	-97		-112	-97		-112	•	
-270	-255		743	-255		-270	-255		-270	-255		-270	-255		-270	-255		-270	-255		.270	-255		-270	-255		-270	-255		-270	-255		-270	•	
-27	-12		-27	-12		-27	-12		-27	-12		193	-13		-27	-12		-27	-12		.27	-12		-27	-12		-27	-15		-27	-12		-27	•	
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-350	-335		-350	-335		-350	-335		-350	-335		-350	-335		-350	-338		-350	-335		-350	-335		-350	-335		-350	-335		-350	-335		-350	•	
- 88	.73		-88	-73		-88	-73		-88	-73		-88	-73		-88	-73		- 88	-73		-88	-73		- 88	. 73		-88	-73		88.	- 73		-88	٠	
25	41		25	41		25	41		25	41		52	41		25	41		25	41		25	41		52	41		301	41		25	41		25	•	
-180	-164		-180	-164		-180	-164		-180	-164		.180	-164		-180	-164		-180	-164		-180	-164		-180	-164		-180	-164		-180	-164		-180	•	
94	-677		-692	-677		-692	-677		-692	-677		-695	-677		-692	-617		-695	-677		-692	-677		-695	-617		-695	-617		-692	-617		-692	*	
-146	-130		-146	-130		-146	-130		-146	-130		-146	-130		-146	-130		25	-130		-146	-130		-146	-130		-146	-130		-146	-130		-146	*	
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-651	-635	*	-651	-635	•	-651	-635	•	-284	-635	•	-651	-635	•	-651	-635	•	-651	-635	•	-651	-635	•	-651	-635	•	-651	-635	•	-651	-635	•	-651	٠	•
570	585	-782	570	585	-782	570	585	-782	570	585	-782	570	585	-782	570	585	-782	570	585	-782	570	588	- 782	570	585	-782	570	585	-782	570	585	-782	968	•	•
357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	357	372	-1256	468	372	-1256	357	•	•
-51	-36	-1329	-51	-36	-1329	-51	-36	-1329	-51	-36	-1329	-51	-36	-1329	-51	-36	-1329	-51	-36	-1329	-51	-36	-1329	-51	-36	-1329	-51	-36	-1329	-51	-36	-1329	-51	•	•
-367	-352	-732	-367	-352	-732	-86	-352	-732	-367	-352	- 732	-367	-352	-732	-367	-352	-732	-367	-352	- 732	- 86	-352	-732	-367	-352	-732	-367	-352	-732.	-367	-352	-732	-367	•	•
-194	-178	.6731	-194	.178	-6731	-194	-178	.6731	-194	-178	-6731	-194	-178	-6731	-194	-178	-6731	-194	-178	-6731	-194	-178	-6731	-194	-178	-6731	-194	-178	-6731	-88	-178	-6731	-194	٠	•
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41		304	4	79	4		1390	41		1406	41		1756	41		2503	41		846	41		1680	41		-51	41		-354	41		1303	41		902	40		-1386	*	
-16.		534	101-	-321	-164		-445	-164		-1907	-164		1110	-164		1326	-164		1560	-164		1592	-164		-386	-164		1017	-164		-3199	-164		-907	-165		-1590	•	
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-130		-1251	- 130	-2517	-130		-1646	-130		- 85	-130		-1870	-130		-1461	-130		-1040	-130		-2147	-130		-994	-130		-68	-130		-1315	-130		249	-131		-394	•	
438	•	- 60	4.5	-838	438	٠	-578	438	•	-297	438	•	-953	438	•	-1883	438	•	-1175	438	•	-839	438	•	-260	438	•	819	438	•	62	438	•	367	440	*	2381	•	0
-635	•	9 6	n *	721	-635	•	353	-635	•	1278	-635	*	917	-635	•	-1559	-635	•	-169	-635	•	-686	-635	•	-1570	-635	•	-797	-635	•	-1900	-635	•	-1081	-636	•	-54	•	•
585	-151	0 1	CBC .	-627	585	-45	-3685	585	-24	276	585	-22	-430	585	-21	-2256	585	-19	-212	585	-18	-3180	585	-17	19	585	-30	-853	585	-14	-2449	585	-11	-1850	584	-23	-841	•	•
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206												-62	-140	206	-99	-1512	206	-49			_				714			986			~		-750	_		_	-991	٠	*
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	-273	- 97		-505	-97		312	-97		-733	-97	•	-806	-97		-959	-97		-252	-97		-164	-97		713	-97		- 928	-97		145	-97		492	-97		-1607	-97		-527	-79		67
	1707	-255		2020	-255		2639	-255		2551	-255		1444	-255		2070	-255		2336	-255		2114	-255		2130	-255		3099	-255		3469	-255		4023	-255		4725	-255		4095	-190		-4649
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	-282	27		-638	27		-639	27		124	27		-270	27		151	27		-379	27		292	27		-790	27		-519	27		-537	27		-985	27		-1575	27		-613	28		-1673
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•	739	438	•	-844	438	*	-946	438	٠	ę,	438	•	-367	438	٠	325	438	•	225	438	٠	1214	438	•	66	438	•	155	438	•	-339	438	*	523	43B	٠,	-314	438	•	-390	427	•	202
•	- 700	-635	•	864	-635	•	1175	-635	*	1073	-635	•	1395	-635	•	884	-635	•	-74	-635	•	-968	-635	•	-992	-635	•	-1244	-635	•	-1296	-635	*	-1789	-635	•	-924	-635	•	906-	-630	•	-261
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	97	, f	-2026	-97		-4659	-97		-1355	-97		-677	-97		-1160	-100		-1771	-101		-1275	-97		-1977	-97		-1560	-97		-4787	-97		-1002	-97		-2407	-97		-687	-97		-1704	- 97
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	190	40.	224	- 54		-227	-54		-69	-54		-240	-54		-250	-57		-608	- 55		70	-54		-24	-54		719	-54		187	-54		-1063	. 54		-464	-54		-816	-54		-1483	-54
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	207	•	299	-73		81	٠7.		4 8	در-		-1269	-73		-852	94-		204	1٠-		465	57-		-842	-73		-598	-73		-513	-73		-540	-73		261	-73		-331	.73		-474	-73
	723	ţ	-1402	41		228	41		-101	41		-152	41		-1375	41		1054	37		-2339	41		-672	41		-3233	41		-883	41		-1840	41		-2671	41		-419	41		-3375	41
	-1972	7 07.	526	-164		395	-164		-187	-164		736	-164		-670	-166		-830	-166		-294	-164		-1032	-164		-425	-164		99	-164		7	-164		198	-164		-112	-164		470	-164
	-3101		-897	-677		-1277	-677		-381	-677		-2413	-677		-5011	-674		-529	-674		-458	-677		61	-677		-1367	-677		-850	-617		-452	-677		367	-677	•	-1324	-677		-1065	-677
	-362	001-	-117	-130		-445	-130		-1062	-130		-227	-130		-274	-128		4-	-127		770	-130		166	-130		1500	-130		7	-130		293	-130		-1443	-130		906-	-130		-430	-130
	-117	*	-496	438	•	305	438	•	-222	438	•	432	438	•	553	436	•	-17	441	*	-111	438	•	93	438	•	395	438	•	687	438	•	926	438	•	1541	438	•	1083	438	•	823	438
	-1219		-332	635	•	-248	-635	*	- 59	-635	•	-538	-635	•	-505	-629	•	-302	-631	*	-637	-635	•	-228	-635	•	198	-635	•	-1232	-635	•	39	-635	•	-169	-635	•	192	-635	•	-310	-635
	-403	-228	245	585	-183	-1255	585	-127	-1771	585	-322	-1308	585	-149	695	582	-305	-1038	583	-511	-569	585	-242	-660	585	-592	-487	585	457	224	582	-829	422	585	-421	301	585	-374	-166	585	-555	-801	585
	308	-2775	-224	372	-3067	162	372	-3565	488	372	-2321	91	372	-3352	583	374	-2391	-277	369	-1744	540	372	-2694	395	372	-1571	20	372	-1880	-222	372	-1194	394	372	-1982	\$51	372	-2132	1160	372	-1648	1543	372
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	237	-732	862	-352	-732	1236	-352	-732	780	-352	-732	709	-352	-732	1905	-344	٠.	1280	-349	٠,5	30	-352	-732	309	-352	-732	-242	-352	-732	518	-352	-732	385	-352	-732	107	-352	-732	684	-352	-732	1276	-352
	865	-4876	1202	-178	-4138	1081	-178	-3129	1690	-178	-3238	1889	-178	-4027	-178	-172	-3116	682	-174	-3526	1474	-178	-6501	812	-178	-7086	-942	-178	-6485	-358	-178	-5937	45	-178	-7334	681	-178	-5367	212	-178	-6348	669	-178
	-3641	-12951	-1857	979	•	-3583		-12890			-12744													-168						156			-1241						-2013		-13101	-771	979
1	206	-50	-140	506	-85	-413	206	-175	-1441	206	-162	-2299	206	- 92	-444	202	-7053	-1570	203	-6940	-1388	206	-16	-1284	206	-1	-2782	206	-16	-715	206	-24	-1964	206	6.	-741	206	-36	-1599	206	-18	-2667	206
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	1 718	-375	493	.1368	843	-982	-1403	-203	-358	-487	-1237	-480	-1005	144	-420	-1125	-856	1123	-645	1899
	- 206		-178	352	-36	372	585	-635	438	-130	-677	-164	41	- 73		-54	27	-12	-255	-97
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	2 944	-868	175	-191	-1040	-693	-3985	16	-116	-405	40		-1126	-424		-1259	-295	1789	-1701	142
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	.74	-12898	-4334	-732	-1329	.1713	-525	•	•											
•	3 1031	.1833	760	-574	œ.	-1164	-1006	- 93	84	-346		-1422		-1159		-1387	237	585	-1714	1339
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	4 1304		1281	-232	-742	-573	-1045	-2587	-814	823	-1455	-328		-1750		-1309	137	-149	-775	1408
	- 206		-178	-352	-36	372	585	-635	438	-130	-611	-164	41	-73	-338	-54	27	-12	-255	-97
	39	,	-5250	-732	-1329	-2560	-268	•	•											
	5 -661	•	802	-320	348	-1315	-510	-44	-76	734	-290	491	-316	-755		-1086	-797	-589	-789	2126
	- 206		-178	-352	-36	372	585	-635	43B	-130	-677	-164	41	-73	-338	-54	27	-12	-255	-97
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-	6 -182	•	1242	315	1420	-1246	-808	-819	-847	- 203	-726	-581	-1886	-280	-515	-620	- 940	£ .	-1223	2430
	- 206		-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-332	.54	27		-255	-97
	-30	•	-5631	- 732	-1329	-37.79	601-		· ;	,		;	;	:		•				
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	- 206		-178	-352	- 36	372	585	-635	43.00	061-	//9-	-104	1 8	٠/٠	-335	•	7	71-	ce7-	
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-	8 -448	742	165	1337	1077	-348	-2262	-1424	-469	-1082		-1518	-54	766	-1385	- 959	-662	-1237	234	2343
	- 206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	4.	-73	-335	-54	27	-12	-255	-97
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٠.	639	-1107	1330	291	-531	-504	-1506	-636	-1249	- 780	-581	537	-204	737	-626	380	414	-1110	134	-422
	- 206	979	-178	-352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
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-562	335		-953	.335		-2405	crr.	458	-335		-2405	-335		-585	-335		734	-338	;	-2310	-335	,,,,,	*/ 77.	333		-2274	۲۲.		9/1	-335	865	-335		821	-335		.1263	-335	;	763		3266.	316		3116	- 4216	2	,	1
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2199	164		-2235	-164		-135	-164	.443	-154	•	119	-164		296	-164		128	. 164		-227	-164		676-	.154		-2103	- 164	;	34.2	-164	- 14 3	-164		-2103	-164		280	.164		2441	107	2005	15.4	* D T :	3,00	2045	, o T	100	100-
2711	643		.157	.611		.1052	-677	a C	-677	•	-62	-677		658	-677		-2747	-677		- 5652	-677	;	7/5	-677	;	941	-611		-2615	-611	. 201	-677		-2615	-611		-148	-611		-2615		25.00	677	9		1662-	10-	100	007.
188	-130		571	-130		- 583	-130	1967	-130	1	1760	-130		73	-130		-1300	-130		151	130		1681-	-130	•	0 5	-130	3	-260	-130	126	-130		1591	-130		1679	-130	•	-1461	001-	2.0		001-	1	חמי ל	067-	0	A O D
391	438	•	.258	438	•	813	438	711	438		.1533	438	•	-1633	438	•	.1633	438	•	-401	438	• (674.	438	. ;	-143	8.	• ;	301	438	-1501	438	•	-864	438	•	-1501	438	• ;	855.	9	101		•	376	200	p •		7.
1227	.635	•	.68	635	•	934	-635	100	5.63	•	-1778	-635	•	190	-635	•	38	-635	•	-642	-635	. (595-	.635	. ;	246	635		. 2574	-635	484	-635	•	673	-635	•	832	-635	•	4 (000	. 2556	303	•	נים	2/8	n •		9107.
379	585	5056	1485	585	.4293	3148	585	11.05	585	-4293	-1485	585	-4293	1117	585	-4293	-1485	583	-4293	-1390	585	865.	PC 1.	585	000	1229	583	. 465	3414	585	1364	585	.465	-1354	585	-465	285	585	.465	914	0 .	604	1 4 4	0 0 0	1	7 9	900	9 00 0	2677.
1652	372	7	. 636	372	- 76	.1125	372	900	372	- 76	-1186	372	94.	-539	372	-76	-1698	372	- 76	.1603	372	-1560	4 1	372	45 PT :	-450	372	-1859	4	372	1567	372	.1859	.756	372	.1859	.1567	372	-1859	-1567	7.5	6291-	173	7 6 6 1	1000	450T.	11.5	1622	A 50 1 -
.554	.35	-1329	42	.35	1329	.257	-36	2010	36.	-1329	-2106	-36	-1329	.232	-36	-1329	-343	.36	-1329	-1329	-36	-1329	57.61.	- 36	-1329	439	97	-1329	1975	-36	. 1075	.36	-1329	-124	-36	-1329	345	-36	-1329	.730	9 9	6761.	25.	95.	777	200	95-	7251.	976
.1315	352	732	2422	.352	132	877	352	20.00	. 152	.732	.773	- 352	. 732	. 578	. 352	732	219	.352	-732	.2327	.352	. 732	56.	.352	25/.	1622.	. 352	. 732	1323	.352	1026	- 352	. 732	96.	-352	.732	-2291	. 352	. 732	- 2291	707	76/.	1	200	20,	. 2233	266.	77.	7777
5.5	178	11030	424	178	11125	.424	.178	200	7 4	.11125	109	-178	.11125	.1065	178	111125	.1240	-178	3636	480	-178	-4965	96/	.178	10958	.2117	178	.10958	2117	.178	191	178	.10958	-2117	-178	-10958	14	178	-10958	-434		55.50	, ,	B/ 1 -		4502.	9/1-	10001-	N N
1217	ć!ó	10080	3549	616	-10125	872	979	07101.	070	10125	552	979	.10125	1429	979	.10125	552	919	10125	1293	616	10001	9621	919	9565	3614	979	8566.	1563	979	9066	979	.9958	1544	979	9958	1949	979	-9958	981	,	3676	2 6	6.60	0000	16%6	7 6	. 5665	7/07
.635	202	ç	525	206	-5	-605	205	7 2	506	2 .	.1484	205	-2	·1864	206	?	-25	206	122	1769	205	4 g	1733	206	7	. 602	206	?	872	206	2.	206	.2	.1733	206	?	-1733	206	ç	-1171	907	57.	200	907	,	1813	907	, ,	9 4 5
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	126	"		1 7		.214	-12		.711	.12	9		77.	-617	-12		-1067	-12	-410	-12		1358	12		.1200	-12		. 12	:	-1060	-12		رد. در	*1.	207	-12		-279	-12		115	-12		ָרָרָי ניי	71.
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	178	.335	1306	-335		35	-335		1144	-335	.633	116		1026	-335		-224	crr.	-854	-335		513	-335	,	67	-335	٥٢-	.335		2405	-335	,	315)	2367	-335		131	-335		2210	-335	70	3,5	3
	858	.73	.274	- 7.3	•	-28	-73		-1145	-73	105		:	1125	-73	į	1,6		201	-73		669	.73		-1083	-73	-1033	.73		-1026	-73	. 6		!	2350	-73		.2143	-73		2143	-73	629		1
	963	3	.841	4 5		.1689	7		-1720	4	.132	1 7	:	-1720	41		07/1-	;	-1720	\$		69.	41	,	- 2030	41	544	4		2206	41	2346	5 5	!	1992	41		- 992-		į	- 166	41	-493	4	:
	1210	-164	714	-164		1286	-164		285	- TP4	930	-164		314	-164		154		532	-164		-1296	.164	,	60.	- 164	-2235	- 164		-2235	-164	37.66	-164		941	-164		-658	-164	3	1991	-164	2235	-164	;
	.2352	. 677	767	-677		-2406	-677	į	-635		145	-677		625	-677	;	663.	•	848	-677		2000	-611	í	5 0	//9-	-2747	-677		-745	-677	922	-677		2709	.617		257	-677		1617		•	-677	
	- 682	-130	.929	-130		-216	-130	;	-379	061.	890	-130		1289	-130		110		265	-130		0,	-130		B	061-	-770	-130		619	-130	-224	-130		- 298	-130		1471	-130	,		051-	٠	-130	
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•	2311	535	-466	-635	•	-210	.635	• ;	573	•	489	-635	•	36	.635	1077	.635	•	.129	-635	•	18	.635	• [17.	•	-719	.635	•	151	-635	.173	-635	•	-178	-635	•	- 777-	-635		366	۲,	970	-635	•
- 258	0601	282	1083	585	. 233	-1144	585	076-	5/11.	.258	1415	585	-258	- 220	585	867.	285	.258	.1175	585	.258	.1175	285	6630	000	4293	1485	585	4293	1485	585	1485	585	4293	-486	582	5089	454	585	2624	100	4243	1485	585	4293
. 251)	1303	2000-	1357	372	-2745	-1357	372	-2143	326	-2513	-1388	372	-2613	-1388	372	6107.	372	-2613	-278	372	.2613	1388		-13							372	•		•		372	. 43	-631	372	'		-76	-844	372	-76
1329	1478	95.	92	-36	.1329	296	95.	6251	975-	-1329	-1796	- 36	-1329	194	95.	194	.36	-1329	.213	-36	1329	53	. 36	1329	34.	1329	2370	-36	1329	. 174	-36	1344 -	-36	1329	1006	9	1329	1019	- 36	181-	3,5	1329	842	-36	1329
732	1234	. 732	46	. 352	-732	1025	246.	757-	55.	.732	. 540	-352	.732	.150	565.	122	.352	732	.1059	.352	.732	1245	355.	1901	. 35.5	-732	9	-352	. 732	373	732	607	-352	-732 .	102		•		245-			-732	2422	-352	.732
1556	240	10569	-812	.178	10641	193	9/1	1,001	.178	10681	.1228	-178	10591	939	9/1.	153	.178	10681	720	-178	10681	154	9/10	19901	178	11125	-888	-178	11125	.1070	111125	.2249	178	4918	390	0.1.	2707	6677	11125	66	. 178	1125	182	178	4995
1856	696	6956-	-750	919	- 96-11	1431	7 1 2		679					181										. 1001			1549		-	1025					-1053	•	-	•	10125			7			. 52101
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-97		200	. 97		026.	,	.1650	-97		-595	- 97	٠	-1713	.97		-23	, ,	-1754	-97		.1813	6	į	1.190	60		1757	ì	516	-97		1262	-97	į	167		-1825	-97		-1825	-97		-1825	-97		-1857	-97
-255		2776	252		. 255		.1808	-255		.1818	-255		-1811	-255		1981	557.	-1912	-255		1971	-255		5.5	255		1915	667.	- 1984	. 255		-2015	-255		-2015	}	-1984	- 255		-1984	-255		-1984	-255		-2015	-255
12		505	12		25.	:	-1566	-12		280	-12		-350	-12		398	71.	-169	.12		330	12		553	. 12		.1673	71.	792	-12		-445	-15	;	613	•	-370	-13		856	-12		-654	-15	į	399	.12
. 14		823	2.1	;	1463	;	-124	27		1536	27		-128	22	i	551	•	1014	27		Şā i	2.7	;	516	2.1		. 1634	•	154	27		1734	27		1734		314	27		1702	27		1108	27		685	. 27
.54		101	75		979	;	818	-54		-156	-54		594	-54	1	5.54	,	-122	-54		155	, <u>5</u> .		477	75.		- 359		069	-54		-12	-54	;	218	5	. 629	-54		898	- 54		723	-54	;	35	-54
335		-653	.335		115	;	343	.335		-107	-335		1952	-335		1942	crr.	-247	-335		27	-335	;	.320	.335		612	677	121	-335		1064	-335	;	2095		1359	-335		653	-335		482	-335	į	21	-335
-73		1447	٤٢-	6	. 23	?	1626	-73		-14	-73		1690 -											987	-73		1129	?	1802	.73		•	-73		, ,		•	-73		-297	- 73		1802	.73		. 20	£7.
41		1334	41		1198	;	-563 .	41		1522	41		658					•			·						34		•	41			41	į	453	;	1688	4		425	41	-	49	4.		1720	1.
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677		2051			7199			-677		2240 -			2293			.2283											875		•				- 677		1562			-677		2405			123			2437	
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. 635	•	2010	.635	•	346	•	.2189	-635	•	345	-635	•	-2252	-635	•	349	45.	-291	.635	٠	579	-635	•	-172	.635	•	-2296	C .	-218	-635	•	237	-635	• ;	354	•	. 513	-635	•	.259	-635	•	-1295	-635	• ;	763	-635
28.5	. 291	1123	585	-400	1199	.295	210	585	.317	.978	585	-308	-1035	585	-260	-1022	285	-1072	585	-585	.1131	585	. 226	-1108	585	- 501	-1075	0 0	-1144	585	-370	-1175	585	.258	-1175	25.	854	585	-233	-1144	585	-233	~	585	-371	-1175	585
372	2451	1002	372	-2047	8111.	-2436	-1181	372	-2340	-1191	372	-2379	-1245	372	-2599	-1235	37.5	-1285	372	-1585	-1344	372	-2785	898	372	-2904	.1288	7 6	-1357	372	-2143	919	372	-2613	1388	-2613	-257	372	-2746	-1357	372	.2746	.493	372	-2140	-1388	372
.36	1329	1025	- 36	-1329	6121	1329	142	.36	-1329	-934	-36	. 1329	1105	- 36	-1329	743	95.	-1693	-36	.1329	.1752	- 36	-1329	1729	.36	-1329	-1696	900	-1367	-36	-1329	-1796	-36	-1329	125	1129	133	.36	-1329	133	-36	-1329	156	.36	-1329	403	.36
352	732	741	- 352	. 732	1942	.732	1356	.352	. 732	1522	.352	-732	1386	-352	-732	-263	- 354	1059	.352	-732	100	-352	732	267	.352	. 732	1306	200	12.12	.352	.732	562	-352	.732	184	213	1088	-352	-132	.105	.352	-732	1571	-352	-732	436	.352
. 178	3915	725	178	0.00	051.	10305	1732	-178	-4242	10	.178	10409	101-	178	-4885	258	10,456	1418	.178	4465	-1894	- 178	5484	265	178	2010	184	0.10	505	-178	10641	.1939	.178	10681	573	0805-	1907	-178	10639	806	. 178	10639	. 663	.178	10639	7	1.78
67.6	9211	. 395	616	.9138	511	9305	1092	616	.9391	2741	979	.9409 -	-637	979	9481	. 627	976	678	979	9535	.737	616	9622	714	919	9592	. 681		750	976	. 9641	-781	979	. 9681	781	1896	-749	919	. 9639	2140	979	9639	-749	919	. 6639	-781	979
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1031	i.	1533	16	-1633	-97		-1633		-666	-97		-1787	-97	1707	.97		.1742	-97		-1685	ĵ.	11711	16/1.		-1671	-97		-426	- 97	-1787	.97		-1754	6	-1682	-97		-1624	-97		-232	-97	101	+ 6 1
1580		1859	255	-211	-255		-1791	CC7.	-1887	-255		666	-255	1045	-255		1439	-255		.1843	\$57.	1 800	. 255		-1829	-255		-1887	- 255	-1945	-255		-1912	\$57.	2612	- 255		1522	.255		67	-255	21676	3
1151	<u>:</u>	541	13	.486	-12		-1548	71.	106	-12		-1297	-12	113	-12		538	-12			71.	141	.12		1463	-12		220	.12	857	-12		- 584	-17	-1597	-12		587	-12		-1393	-12	916	2
396	,	52	27	1238	27		-1510	,	4.8	27		0.0	27	.1111	27		-1618	23	:	-1561	7	101	27		-931	27		468	21	86	27		-189	,	-767	27		-362	27		-1354	27	~	1
. 241	5	.70	.54	323	-54		- 582	ń	523	-54		210	-54	001	-54		.1699	-54	i	9 1	10-	.681	-54		.271	-54		.	-54	566	-54		1208	, ,	642	-54		98	- 54		320	- 54	1001	*
-1088		-1871	.335	906	-335		-672		-1264	-335		-2025	-335	81.8	-335		-276	-335	!	-425	cer.	.1412	.335		-886	-335		-1967	-335	-1447	-335		-1394	655-	-1920	-335		86	-335		297	-335	.1756	1
987	?	162	.73	537	.73		100	?	109	.73		-874	.73	958	.73		.1718	-73	;	-1661	:	90	-73		-112	-73		-1705	-73	229	-73		-1730	· .	1107	-73		-193	.73		1256	.73	211	:
1558	;	1495	41	.1496	4		1351	;	. 6-	. 1		970	7	Ş	41		1331	4	:	-1547	,	1594	-11334		.1533	4		191	\$	-115	41		-1617	7	393	41		325	41		.833	41	.1381	
.1763	t 0.7	.1700	-164	-1700	-164		125	7	-1796	-164		-1854	-164	-	-164		-52	-164		180	70.	1207	-164		238	-164		-301	-164	-855	-164		. 65	194	-1749	-164		1087	-164		-1545	-164	-1585	,
788		-2213	-677	-2213	-677		. 2213		685	-677		-2367	-677	.2167	-677		-2322	-677		-2265		1116.	-677		316	-677		1170	-677	-2367	-617		1484	14	-2262	-677		-2204	-617		-2058	-677	.2098	,
-383		1592	-130	1	.130		832	061-	765	-130		1416	-130	.2.	-130		666	-130	:	135	061.	296	.130		-91	-130		21	-130	-1820	-130		-1787	061-	296	-130		- 109	-130		-186	-130	79	:
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	-508	-164	:	164	:	-2060	-164		-2465	-164		-1631	-164		-3562	501-	-2265	-164		-2020	-164		-4194	.164		-1893	- 164	3501.	-164		-1114	-164		799-	* 01.	-2301	-164		-804	-164		-79B	-164		.2046
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	-1256	-130		-130	•	-642	-130		198	-130		-581	-130	;	19:	. 130	\$76	-130		-110	-130		. 545	-130		-229	- 130	-	.130		773	-130	ć	110	201	1132	.130		1331	-130		.106	-130		307
•	-1075	438		43.8	•	-1033	438	•	-1284	438	•	-2043	438	• ;	- /34	•	-1261	438	٠	-1694	438	•	-3592	438	•	~ ;	4.38	- 303A	438	•	-268	438	• 6	43.6		-934	438	•	- 980	438	•	352	438	•	1325
•	-586	-635	ָּרָנָי [ָ]	-635	•	-215	-635	•	-453	-635	٠	-872	-635	• 6	01/	•	721	-635	•	1199	-635	•	826	-635	•	957	-6.45 -	45.0	-635	•	792	-635	• 0	6.26		-123	-635	•	-1678	-635	•	1273	-635	•	363
.25	-448	585	125	282	-24	17	585	-49	217	585	-61	459	285	-22	9 20	.32	-556	585	-20	1393	585	- 5	2049	585	-13	1759	n 0	1430	585	.32	-216	585	-16	585	-25	19	585	-14	- 56	282	-22	-1900	585	-12	.1602
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-25	-719	206	-38 -	206	- 18	-292	206	- 60	- 944	506	- 47	-336	907		206	. [9]	-526	206	-21	7	206		. 324	506		247	200	1101	506	-104	498	506	. 69.	506	-118 -	404	506	- 199	. 573	506	.133 -1	322	506	- 337	261
	196		197	•		198	•		199		' ;	200		, 102	;	•	202			203		, ,	507			502		206	,	•	207		208			509	,		210			211			212

.6.		. 386	.97	Š	5 6	· .	926			2316	. 6.	•	589	. 97		879	<u>,</u>	, 00	. 63	ñ.	9	200	î.	101		Š.	286	.97		367	. 97	901	. 6.	;	660	- 64		.352	.97	i		٨.	7.3	5	ì
.255		-1166	-255	,	900	667.	.268	.255	}	•	. 255		-465	-255			567-	•	256		2712	376.		1776	236.		4712	-255		4736	. 255		- 255			-255		. 4730			7 1	007	1304	.255)
.12		.835	-13	603	7 60	71.	378	.12	;	151	.12	:	82	12		<u>.</u>	71.	1032			,	3 :	:	196	; ;	:	•	12		. 190		•	. 12			-12			-12				•	- 12	
7.2		691	27	000	200	•	83	27	,	148	27		-95	27	;	776	Ì	1253	7.	;	1364	,,	:	177	,,		1.186	27		-563.	1.7	13	2.2	1	-565	2.7	;	-752	27	•			_	27	
ş		2296	.5.	1366.	75.	5	-214	.51		.864	.54		110	-24	:	911	, 1		-54					-879		;	•	-54		-517	ř	1318	-54		- 698			/2/		636	200	;	730	. 5	:
.335		-1744	.335	-1155	500		- 397	-335		-1017	-335		1082	-335					-335		536	-335	:	-147	-335		1355	-335		843	crr.	•	-335		9	-335		1 65		613	3 2	?	. 547	335	
٤٢٠		. 560	.73	87.6.	.73	•	-1337	-73		-821	.73		282	٠7.	;		?	801	.73		1282	.73		988	.73	٠.	675	.73		822	?	262	٠73		691	.73	6	2 6	۲.	276	;		1629	.73	
;		. 3756	-	.2856	7		-4457	Ŧ		-2854	43		-2569	41		7 7	:	-2086	4		4439	1.4		.2033	4.1		3705	41,	;	-526	÷	-342	4.		-713	4.1	,	9571	7		; =		•	41	
-164	;	.2063	91	.2053	-164		-2611	-164		.703.	-164		-361	-164	9	1,64		611	-164		-154	- 164		Ċ	-164			-164	į	-678		4	-164		115	-164	1307		7 07-	202	-164		-445	-164	
11.9.	;	3 5 6	19.	438	.677		152	-617		1952	-611,		2371	-677	3716	-677		642	-617		1377	-677		1856	-611		1160	-677		75/		.1222	-677		-635	-617				392	.677		341	-677	
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138	• •	6671.	7	-1445	438	•	-1093	438	•	-684	438	•	-576	438		438	•	-448	438	•	416	438	•	37.1	438		164	438	• 6	42.4		1036	438	•	203	438	274		9.	-28	438		-724	438	•
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206	917	206	-12	936	206	-14	007	206	0	-91	506	6	152	9 0	665	206	-12	-576	206	۲-	.1409	506	-22	2539	506	7	.17	206	-299	206	-15	-1758	506	9 ;	, ,	. 23	.825	506	0	-1438	506	Ś	- 598	506	
•	163	•	٠	164	•	•	165	•	• ;	166		٠ ;	167	٠.	168	•	•	169	•	•	170		•	171		•	172	. ,	173		•	174	•	. 1	1		176			177		:	178		•

3.0	- 66		66	.97	0.01	610.	į	2196	- 97		3057	.97		.988	-97	9001		;	518	-97		.952	.97		4.7	.97	:	-868	À	282	-101		-1740	- 36			- 701	376	2	;	889	-97		195	.97
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-1522	-75		.77	τ.	-1347	. 23		-1815	.73		- 849	-73		176	- 13	22	-73		127	-73		-173	.73		516	.73	,	29.	?	1051	99-		1108	99-	Ş	3 5	•	-590	.73	1	-903	.73		-549	٠٦3
1709	46		182	7	968	4		-853	41		142	41		- 164	7	1906-	. 4		-1867	7		-832	41		-775	41		-1484	;	-562	38		558	~ ~	6	9 5	,	1293	4	:	1198	41		1030	7
-659	.164		-1929	-164	, q	-164		-715	-164		-196	-164		-166	-164	. 978	.164		-559	-164		-843	-164		-1562	-164		. 164		520	-162		-697	-160		171	101	. 192	-164		16	-164		-1632	-164
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-662	-130		649	-130	215	-130		851	.130		1276	-130		641	-130	1048	-130		-118	-130		28	-130		-265	.130		.130		.1291	-133		-532	-135	0001	6071-		.1729	.130		-1899	-130		-1255	.130
-494	436	•	-473	438	e G	438	•	358	438	•	40	438	•	281	438	-241	438	٠	225	438	•	697	438	•	189	138		0 6	*	648	440	•	443	440	• 6	777	•	-1080	438	٠	- 444	438	•	-1382	438
-149	-635	•	588	-635	987	.635	•	286	-635	•	206	-635	•	328	-635	635	-635	•	287	-635	•	-93	-635	•	511	-635	. 20		•	-594	-635	•	-830	-634	• :	(17.	3	.319	-635	•	142	-635	•	72	-635
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539	-33	-8751	304	-36	456	-36	-1329	619	-36	-1329	1011	-36	-1329	1566	95-	1563	-36	-1329	1059	.36	-1329	1191	36	1329	2232	. 36	6761	36-	-1329	-2871	-38	-8697	-444	24.	-8630	25.	-8604	-864	-36	-1329	.2762	- 36	-1329	.2023	.36
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739		•		-17B		-178	-6732	-416	-178	-7542	-176	-178	-7240	-64	-1/8	-623	-178	.14063	-692	178	.7549	32	178	7315	619	176	0 5 70	-178	-6396	-1296	-182	-6935	63	6.1.	. 425	72.	-6432	-32	-178	-6139	-527	-178	-7387	196	.178
-28	975	-27	-721	13051-	-27	979	-13054	80		-13042			-13063	-1716	213055	1303	979	-13063	29	979	13063	985	616	13055	1173	616	9707	976	-13026	1711	979	.20	1486		924	. 68	-	901	979	-12913	1168	919	-12920	1577	979
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129	•	•	130	٠.	131	٠	٠	132	•	•	133	•		134		135	٠	٠	136	٠	٠	137		•	138				•	140	٠	•	14	• .	142	·	•	143	٠	٠	144	•		145	

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	161.	-97	0.661.	. 67		.111	.97		. 355	6.	:	307	.97		979	- 97		32	98	;	6		1460	.97		2003	.97		996	.97		1085	.97		-818	6.	-202	.97		-557	- 97		169	. 97		245
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	357	2.1	1005	27		715	27		1212	56	1	710	27		949	27	į	2.10	30	9		ì	117	27		973	27		1090	27		230	27		667	?	678	27		674	99		7	2.1		192
	-1476	Š	- 504			-381	-54		- 97	-49		-289	-54		385	-54	;	- 343	- 54	903	3	5	- 95	-54	:	-2636	- 54		-841	-54		-521	-54	į	194	r n	.351	-54		-483	-60		-471	-54		21
	- 78	- 335	82	-335		-1228	-335		.161	-335		-465	-335		-444	-335	į	571	-333	79.	22.	,	10	-335		943	-335		1119	-335		323	-335		1575	crr.	1134	-335		1368	-255		1752	-335		961
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	810		366	-677		228	-677		-134	-668		1118	-677		-566	-617		0/01-	-671	.773	.677	•	405	-677		-635	-677		-58	-677		456	-611	į			-199	-677		-1570	-685		-274	-611		- 766
	906-	051-	170	-130		187	-130		-199	-128		-202	-130		-823	-130	3	96/	-132	.101	0,1	:	100	. 130		122	-130		-353	-130		215	.130		315	061-	829	-130		995	-150		-1648	-130		-138
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	956	0.0	-179	-635	•	16	-635	•	451	-634	•	-918	-635	•	7	-635	. ;	506.	-633	184	-635	•	.183	-635	•	.144	-635	•	712	-635	•	240	-635	• ;	7 ;	•	-453	-635	•	223	-613	•	102	-635	•	164
•	-1105	0 0 0	-140	585	-56	-282	585	.138	-927	581	-59	146	585	-139	1113	585		-1063	280	909	28.5	- 94	.291	585	- 85	640	585	.119	885	582	-82	1035	585	-148	1212	-46	-16	585	-117	415	900	-80	842	585	-210	1530
	-3394	3/5	-3716	372	-4707	-1683	372	-3451	-3729	367	-4647	-1582	372	-3445	-1960	372	0560	990	941 ye		372	.3987	1659	372	4128	.1165	372	.3658	-1096	372	-4175	-2313	372	-3354	9976-	-4985	-1563	372	-3678	-2397	337	-4215	-2136	372	-2887	-1578
	605	95.	-81	-36	-1329	-797	36	-1329	.1638	-39	-8536	-2062	-36	-1329	-1399	-36	6761-	¢,	22.8.	9 6	3.6	1329	882	36	1329	259	. 36	-1329	41	-36	-1329	206	- 36	-1329	262	-1329	-313	-36	-1329	1213	-41	-106	829	-36	-1329	517
1	477	725	4	-352	-732	802	, 352	-732	1207	-345	4-	939	-352	-732	813	-352	757	1340	7	297	35.2	732	85	352	732	543	352	-732	-1098	-352	-732	-514	-352	.732	87.	-732	157	-352	-732	9,6	-296	-3815	265	-352	-732	-626
	96.	.6667	-178	-178	-7632	-238	.178	-7632	470	-177	-13855	959	-178	-6539	43	.178	007/-	7/5	111.	168	178	9.69	1254	. 178	5636	53	178	-6046	-332	-178	-4650	-507	-178	-4625	65.6	-5614	-1074	-178	-4428	-1185	.169	13660	.1651	-178	-6770	- 985
		27861-	1435	979	12843	1031	979	-12843	1325	975	-10	811	979	12819	-1142	979	FC07T.	11/3	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	265	979	12798	67	516	12795	968	616	12785	-1069	979	12795	288	979	12746	200	12709	-581	919	12689	1153	951	=	-245	979	12922	111.
	-1327	- 14	-347	206	- 7	-1095	506	.7	-1526	202	-7255	-1157	506	-19	-221	206		, , ,	507	-107B	206	.23	443	206	.24	.607	206	.22.	-1064	206	- 65	-1054	506	. 09-	99/7-	- 30 -	-1561	206	- 69-	-2015	151	- 2060	-1499	506	-13	-3051
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910	666	105)	-315		-14	-335	}	496	-335	:	106-	.335	,	-1315	-335		-1522	-335		179	- 335			.335		521	-335		640	-335		959	- 335	177	, ,		•	.335		•	-335		538	-335		197	.335	
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	1411	27		-439	27		- 94	27		2	27		904	27	1.36.1	22		1126	27		1087	27		. 189	27		-1162	27			;	-128	27		-925	2.1	1	271	27	;	568,	5.2		.86	27	;	37
	.2899	.54		-1172	,54		-910	.54		-437	.54		-862	-54	917	2.5		-1094	.54		-834	.54		-1370	.54		-1640	\$	03/11	60/1	;	.924	.54		-2719	4.2		-832	.54		1609	.54		-587	.54	;	.163
	-1448	-335		-2870	.335		- 76	.335		-1777	-335		-1129	-335	373	33.5		-239	-335		-259	-335		-67	-335		797	- 332		33,5	;	1312	-335		375	- 335		1165	.335		- 3005	. 335	;	-602	.335	4	.775
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	1955	-164		1029	.164		-192	-164		569	-164		9	-164	100	-164		-697	-164		476	-164		-131	-164		1388	-164	623	196	5	-237	-164		1011	-164		1197	-164		1197	-164		136	-164	į	\$21
	- 2342	-677		201	-611		783	.677		1458	-677		729	-677	000	.677		1187	-677		1047	-677		1306	-677		1373	.677	977	5677		1468	-677		3055	-677	;	1923	-611	. ;	2531	-611	•	-187	-677	:	1360
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13683	- 923	-178	13697	- 969	-178	13706	467	-178	13708	148	-178	13716	-151	-178	-7541	4,1,	-7439	-98	-178	.7544	296	-178	13707	1804	178	13770	913	178	13815	170	13845	-4706	-178	-5403	-166	-178	-6077	-1509	-178	13801	-2255	178	0.96-	-1290	-178	. 7660	.2319
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000	.12		-1754	-12		.777	-12		- 92	-12		-167	-15		-99	.12		-1762	.13		-1817	-13		-433	.12		-1439	-15		-1650	-12			;	-1099	. 12		- 869	-12		-30	-15		-168	-13	•	7	.12
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ć	-73		-192	. 73		-23	-73		220	.73		183	-73		689	.73		-833	-73		920			1272	٤٢٠		395	-73		1401	-73		1484	?	157	.73		545	.73		707	-73		1281	.73		2493	.73
	7071		-1599	41		64	41		489	41		236	43		618	41		671	4		-215	43		694	\$		710	7		301	4	;	2	;	-131	41		-227	\$.109	ţ,		7	41		.125	7
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	-677		-154	-677		.1407	.677		34	-617		1054	-611		1452	-677		-854	-677		-365	-611		.1035	-617		.848	-611		-1630	-617	,	100	9	901.	-617		1270	-611		897	-611		474	-611		-1663	.673
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3371	438	•	-187	438	•	-620	438	•	288	438	•	106	438	•	-269	438	•	-343	438	•	549	438	•	-237	438	•	1210	438	•	197	438	• ;	946	•	-130	438	•	-972.	438.	•	-2064	438	•	.1905	438	• ;	.1603	138
1020	.635	•	-1349	-635	•	218	-635	•	1476	-635	•	1114	-635	•	689	.635	•	-885	-635	•	-207	-635	•	-164	-635	•	235	-635	•	- 565	-635	• :	7.	•	850	-635	•	1987	-635	•	626	-635	•	1475	.635	•	-466	635
1000	585	-46	-1444	585	-25	-380	585	-39	-373	585	-24	-2831	583	-38	-419	585	-30	566	585	-39	-131	585	. 76	1049	282	. 80	.1270	585	-60	-467	285	- 56	7 6 6 7	. 96	168	585	-71	-1626	585	-3	-1715	585	-31	-422	585	-37	.250	282
316	372	-5009	-1027	372	-5885	-114	372	-5244	-312	372	.5910	-493	372	-5278	1200	372	-5604	443	372	-5239	1079	372	-4284	235	372	.4516	.492	372	-4616	.58	372	-4705	5101.	-4139	.771	372	-4382	1001	372	-5575	-286	372	-5569	- 754	372	. 5267	32	372
ticc	-36	-1329	158	-36	-1329	754	-36	-1329	-357	-36	-1329	815	- 36	-1329	-2090	- 36	-1329	159	-36	-1329	192	-36	-1329	-586	.36	1329	156	. 36	.1329	88	-36	-1329	960	-1329	947	-36	-1329	-71	- 36	-1329	322	-36	-1329	-1721	.36	-1329	.1220	. 36
6	-352	-732	-1340	.352	-732	-1391	-352	-732	-641	-352	-732	-1368	-352	- 732	-213	- 352	- 732	163	-352	-732	- 191	- 152	-732	112	352	732	1106	. 352	-732	- 941	.352	-732	188.	- 732	-217	-352	-732	-275	-352	-732	-1453	-352	.732	-835	-352	.732	903	352
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. 352	732	.1179	-352	-732	-1179	-352	.732	-787	- 152	-732	-1461	.352	.732	2197	-352	-732	2230	-352	-732	2230	-352	-732	-543	-352	-732	.254	-352	-732	.254	-352	-732	-547	.352	-88	. 1234	.352	-732	. 68B	700	132	h171.	.325	. 732	-1180	-352	-732	-838	-352	732
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. 86.5	3	;	.743	5.	.	-407	-54		-184	-54		-410	7.		-844	15.		-1145	5.54		416	-54	:	.207	8.5	;	0.4.	:	5	-1145	-54		-1145	-54		-322	-54		-267	-54		-199	-54		-702	-54		-719	-54
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717		•	.1155	.73	!	1769	-73		1155	-73		-1164	.73		-1164	.73		-1164	-73		-1164	.73	ı	-738	.73	•	224	; ;	?	-637	. 2.		224	.73		-1164	-73		-1164	.73		-1164	.73		439	-73		1164	-73
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3445	.677		99	-611		-1759	.617		618	-677		-401	-677		-1768	-677		969	.677		-689	-677		.1768	-611		-1768	.677		-1768	-677		-1768	-677		-1768	-677		-1768	-677		-689	-617		-1768	-677		1758	-677
- 369	- 130		.992	.130		.953	-130		-886	-130		.1221	-130		-895	-130		-479	-130		.597	-130		-1221	-130		878	.130		-250	-130		1701	-130		966-	-130		-774	-130		-1221	-130		-218	-130		1221	-130
-456	438	•	- 381	438	•	. 249	438	•	-645	438	٠	-420	438	•	2150	438	٠	1418	438	•	2186	438	•	905	438	•	-140	438	•	-438	438	•	1825	438	•	2222	438	•	-416	438	٠	2177	438	•	33	438	•	-310	438
-1718	535	•.	-1718	-635	•	-297	-635	•	2259	-635	•	- 965	-635	•	23	-635	•	-856	-635	•	-742	-635	•	-1726	-635	•	2094	-635	•	1424	-635	•	-1343	-635	•	-1726	-635	•	-633	-635	•	.1057	-635	•	2048	-635	•	2245	-635
751	585	-101	-497	585	-101	-497	585	-101	278	585	- 294	662	585	.101	- 506	585	-101	- 506	585	-101	-506	585	.101	-506	585	-101	-506	585	.101	215	585	-101	- 206	585	-101	- 506	282	-101	- 206	585	.101	- 206	585	-101	0	282	-101	905-	SHS
-710	372	.3892	.710	372	.3892	1975	372	. 3892	-493	372	.2441	-468	372	-3883	- 719	372	.3883	-163	372	-3883	-719	372	-3883	-719	372	.3883	-719	372	-3883	-719	372	.3883	-719	372	3883	-402	372	3883	-113	372	3883	-719	372	3883	-719	372	3883	-719	3 / 2
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	-130		-512	-130	•	1040	OFT-	-358	-130		-476	-130		976	25.1.	242	-130		-512	-130		-525	-130		-850	-130	;	-629	-130	-525	-130		- 50	-130	-867	-130		908	-130		-264	-130		-121	-130	
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	372	4163	- 348	575	-4183	966	-4183	-348	372	-4183	-348	372	-4183	-348	372	- 108	372	-4183	- 348	372	-4183	-348	372	-4183	-136	372	-4183	- 348	372	348	372	-2068	-710	372	-395	372	-3892	-538	372	-3892	-710	372	-3892	.710	372	-3892
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	-178	7 000	1726	-178	- 9044	668-	-1/8	468	-178	-9044	-352	.178	- 9044	136	-178	668	-178	- 9044	.517	.178	.9044	-839	.178	-9044	662	.178	- 9044	.332	-178	-517	.178	- 9044	-878	-178	1943	-178	-9719	-383	-178	- 9719	-1261	-178	. 9719	-1261	-178	-9719
	979	8044	1770	919	-8044	824	-8044	1775	979	-8044	259	979	- 8044	765	979	259	919	-8044	259	979	-8044	824	616	-8044	716	616	-8044	1242	979	765	979	-8044	621	979	-103	979	-8719	-103	919	-8719	3840	919	-8719	1001	.616	-8719
	206	SO	-514	206	φ.	260	50¢	514	206	8,	-514	506	φ.	.514	506	.514	506	89-	260	206	æ	.514	206	8	-514	206	6 0	1450	502	.514	206	87	-817	206	-877	206	è	-262	206	Ş	- 556	206	φ,	-877	206	'n
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	60	255		-884	-255		- 950	-255	400	200	£ 22	. 984	-255		-984	-255		-975	-422	90	250		. 975	.255		2305	-255		089	-255	200	. 256	}	-975	-255		-975	-255		- 975	-255		- 975	-255	- 975
	. 662	17		.641	.12		.293	.12	1761		71.	.741	-12		.121	-12		-732	71.	.403	20.	:	18	.12		.732	-12		247	-12	.,,,	-13	:	-732	-12		1572	-12		-12	-12		-732	-12	-732
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	180	'n		430	.5.		-750	-54	. 20.	7 4 4	5	-484	-54		.783	-54		1414	ř.	6.50	קר		.774	-54		-774	-54		-470	-54	2774	.54		-774	-54		-774	-54		-774	-54		-159	- 54	+17-
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	184	.73		-252	.71		299	-73	.281	17.	3	-351	.73		8	٠٠.	į	5.6	?	125		•	- 793	-73		96	.73		299	.73	8	- 7.3		- 193	.73		817	-73		213	-73	:		-73	076-
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	-395	617		-234	-677		-1372	-611	2654	-677	•	2654	-617		-1405	-677	ć	100	;	3252	-677		-1397	-677		.1397	-677		440	677	545	-677		-1397	-677		-1397	-677		-1397	-617	Š	586	//9-	1255
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-1329	-230	.36	1329	-665	.36	-3111	25).	1329																						1329													.36	-1329	.756
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4.1		1587	7	.388	41		-742	41	;	703	41	-434	1	:	.812	41		-552	4		296	4.			41		- 720			- 720	41		- 108	41		4		·	41		290	14		. 290		
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677		250		.764	-617		1522	-677		1522	-677	-114	-677		•	-677		1534	-677		-1515	-677		1483	-677		1437	-613		1437	-677		. 1426			- 677			- 677		•	- 677		1307	•	
-130	i	-544	061.	1018	-130		869	-130			-130	- 769	-130		•	-130		470				-130		•	-130		1197 -			- 269			274		٠	-130		·	-130		358 -			-513 -1		
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	269	.12		89	12		.375	-12	ę	,	-12		-238	-13		203	-12		-862	-12		103	-12		· 794	.12		.383	.12		.440	-12		.172	-12		-365	-12		-824	-12		-64	-12		-416	-12		146
	7	23		1821	23		-348	27		107-	2.3		677	27		-671	27		1640	27		-53	27		408	27		1570	27		-356	22		9	27		122	27		-88	27		1926	27		-36	27		97
	1419	.54		215	.54		197	-54	ć	, i	-54		92	-54		-575	-54		424	-54		476	-54		335	-54		.281	-54		1464	-54		264	-54		-461	-54		-579	- 54		83	-54		-93	-54		-416
	221	335		- 98	-335		-358	-335	٠	7 ;	- 335		-1020	-335		-1117	- 335		1126	-335		-581	-335		563	-335		-450	-335		444	-335		623	-335		159	.335		-136	-335		629	-335		-830	-335		-619
	520	7.3		.112	.73		۲,	.73	,	605	-73		.758	.73		-19	-73		- 923	-73		1998	-73		219	.73		-435	-73		-47	- 73		. 357	-73		-952	٤٢-		1701	-73		-466	-73		1766	£.		250
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	-416	-164		-848	.164		-103	- 164		96/1	- 164		-419	-164		-1006	-164		-1014	-164		- 706	-164		-1044	-164		107	-164		-1044	-164		-937	-164		-937	-164		959	-164		-1022	-164		-581	-164		- 974
	-1362	.617		-1360	-611		-1362	-677		7961-	.611		-1362	-617		-1518	-617		-1526	-677		-1539	-677		-1556	-677		-1556	-677		-1556	-677		-1556	-617		-1556	-611		-271	-677		.574	-677		-1495	-611		-525
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-80	23	585	- 90	. 99	585	-84	293	585	Ē :	114/	585	-81	-100	585	-193	215	585	- 95	208	585	- 99	1176	585	-106	-294	585	- 90	-294	585	.90	795	585	-90	-294	585	- 90	-294	585	- 90	-294	585	- 90	-272	585	-89	-233	585	- 86	-224
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. 1965	294	979	-1965	295	979	-1961	294	979	- 7963	294	979	- 1963	167	979	-1963	137	979	-9283	710	979	-8538	117	979	-8322	100	979	-8352	100	979	.8352	100	676	-8352	819	979	-8352	816	979	-8352	1351	979	-8352	122	979	-8310	161	919	-8236	2587
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i	925	1	.908	.255		- 908	-255		-886	-255		-916	-255		-877	557.	-912	-255		-912	-255		950	255		950	255		-939	-255		.939	-255	6	.255	}	-953	-255		-948	-255		- 940	-255		- 940	-255
,	262	:	-405	.12		- 665	-12		1661	-12		-390	-12		-353	71.	-670	-12		106	-12		345	.12		7.08	12		.469	-12		135	-12	303	-12	;	-447	-12		-368	-12		1549	-12		-302	-12
:	165	;	151	2.7		-318	27		-296	27		-12	27		-248	17	.83	27	•	-382	5.2		849	27		246	2.7		-657	. 12		-165	27	* * * * * * * * * * * * * * * * * * * *	27	ı	1861	27		-160	27		-32	27		-82	27
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	861.	;	986.	-335		-988	-335		-237	-335		1853	-335		-179	crr.	104	-335		699	-335		.405	.335		-685	-335		-145	-335		20	-335	,	-335	:	-717	-335		1666	-335		-593	-335		474	.335
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	5.5	•	.1289	-635	•	-570	-635	•	-1267	-635	•	-1297	-635	•	-1258	6.0	-550	.635	•	-757	-635	•	-514	-635	•	-219	-635	•	. 193	-635	•	414	-635	. 857	-635	•	-629	-635	•	-1328	-635	•	-1321	-635	•	-653	-635
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.5.		: 3		-247	-54		476	- 54		-36	- 54		-480	-54	910	1 1		-240	-54		-532	-54		-440	.54		-448	-54		-356	-54	171	12.		-208	-54		- 566	-54		121	-54		- 66	- 54	
135	200			.526	.335		-513	-335		-386	-335		- 997	-335	9	.335		-242	-335		-253	-335		-551	-335		179	-335		-222	. 335	- 294	-335		-308	-335		-401	-335		-960	-335		- 660	-335	
13	0	. .	,	.756	-73		624	-73		-735	-73		-735	.73	,	.73		332	.73		2178	-73		- 74	.73		632	-73		-171	-73	342	. 7.		290	-73		-789	-73		-783	-73		-401	-73	
0.5	5		:	1907	Ţ		376	41		465	41.		928	ţ	20,10			53	\$		-564	\$		-327	41		130	43		-653	7	674	41		-312	41		-390	41		-669	41		259	41	
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438	2	2 6	•	653	438	•	-225	438	•	-225	438	•	577	438	• 6	438	•	120	438	•	260	438	•	-39	438	•	-211	438	•	526	438	. ī	438	•	'n	438	•	-46	438	•	-41	438	•	7	438	•
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		717		214			215	,	٠	216		•	217		. ;	9		219			220			221			222			223		25.6	,	٠	225	•	٠	226			227			228		•

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	4			.222	-12		-453	-12		-341	-12		-630	-12		-341	. 12		-188	-12		.83	12	:	ć a y	-	:	6.6	2		-691	-12		53	-12	;	.153	-17	109-	; ;	4	-282	2۲-		-252	-12		-664
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	. 117		•	60	- 54		- 905	. 54		-594	.54		.938	-54		1598	-54		-403	- 54		.452	5.	;	359	75.		115	15.		-733	-54		-259	-54	;	65.	e 0	.563	8 5	;	-341	-54		-724	-54		1740
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	1708	73			.73		. 923	.73		-285	.73		1935	.73		. 500	٤٢.		45	-73			.73		-77	.73	ı	-326	-73		-752	-73		.752	.73		345					•	.73			-73		- 725 · ·
	4.3	: =		0	ij		-412	41		-407	41		-446	£		144	7		908	41		-830	41		630	4		183	‡			41		2174		į	100	;		1.4		133	41		-277	41		- 99-
	.611	.164		1954	-164		1850	-164		1015	-164		-133	-164		-391	.164		1035	-164		631	-164		. 765	.164		20	.164		.57	-164		-843 2		;	616	F 0 1	843	164		Ċ	-164		-401 -			-118
	1527	. 677		1504	-617		.1527	.677		•	-617		1103			- 272			-1548 -1				. 677			. 419-			- 677		-392			7			673		- 392				- 677 -			- 677		- 22-
	•	130		•	-130		-350 -				-130		-756 1			-159			1001			-1001				-130 -			-130 -		-411 .			-589			200			130		1286 -1			-425 -1			. 741
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		438		-203			-413			1606			171-			-445	43	-	1586	43.	•	7	438	·	.233	438	•	-233	436	•	-23	438	•	-211	438	. 241	4.4	;	-241	438	•	102	438	•	106	438	•	-214
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517.	121	.352	. 732	1180						_	.352						.352																		265												-732	
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	481									187							506																								•			•	-464		•	
	196	1		197			. 86 1			199		٠.	•			201	•		707			203			204	••		505			206 .4			207	. ,	208 -4			209 -4	- 3		210			211 -40	· `		712
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16		655	.97		117	- 97		-836	- 97		-836	-91		-836	- 97		.836	- 97		-836	- 97		.847	.97		270	.97		077.	- 97		077.	-97		-770	-91		26,		-770	. 9.4		.756	-97		-485	-97	
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12		103	~		- 324	-12		-752	-13		-752	-12		-487	-12		-752	-12		-335	-15		. 763	-12		-685	. 12		989	-12		-686	-12		- 98	-12	,		:	-277	-12		-671	.12		-671	-12	
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C.		٠,٠	7		.644			-613	.73		.813	.73		-17	-73		-613	-73		-301	.73		-824	. 7.3		.746	73		-746	73		93	.73		1978	-73	;	77	•	136	- 73		-732	-73		- 732	-'73	
7		:3:	-		.531	7		ó 65·	4.		669.	÷		1688	43		669-	43		-385	41		-302	4.		-633	41		-633	41		-633	41		-633	41	3		:	312	41		-114	41		-618	41	
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438	•	297	438	•	-133	438	•	-302	436	•	327	438	•	-305	438	•	121	438	•	-302	438	•	966	438	•	-236	438	•	-20	438	•	1862	438	•	229	438	. 201	4 3 8	•	1829	438	٠	480	438	•	10	438	•
. 615	•	-1205	-635	•	367	.635	•	. 590	-635	•	-1375	-635	•	966-	-635	•	-142	-635	•	- 855	-635	•	-1386	-635	•	-1309	-635	•	1784	-635	•	-843	-635	•	-1309	-635	9.0	-615	•	.628	-635	•	916.	-635	•	-1294	-635	•
585	17.	7.	585	.77	685	583	-202	424	585	-83	745	585	-83	408	585	-83	260	585	- 63	653	585	-91	869	585	-103	788	585	-80	-89	585	-80	334	585	80	1737	282	ניני	282	- 80	489	585	-80	1371	585	-80	490	585	-80
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352	732	520	.352	. 732	1350	352	. 732	37	352	732	205	352	.732	164	352	732	.360	. 352	-732	191	. 352	.732	. 17	- 352	732	176	. 352	.732	.610	352	-732	.170	.352	. 732	116	. 352	1026	. 352	.732	.29	.352	.732	-650	-352	-732	-490	-352	-732
.178	8105	. 750	.178	8705	. 750	178	. 4234	1636	.178	-9085	.918	178	. 9085	.825	178	.9085	. 432	-178	- 9085	6.0	.178	9085	1698	.178	2777	652	.178	8943	852	.176	.8943	-567	.178	. 8943	- 764	9/1/8	C P G -	.178	. 8943	.852	-178	.5400	1757	-178	-8912	7	.178	-8915
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		163	•	•	164	•	•	165		•	166	•	•	167	•	•	158	•	•	169			170			171			172	•	•	173			b / C		175			176		•	117		•	178		•

243	Ç,		a, a,	66.		119:	- 61	;	19.	- 97	;	-614	, ,	965.	-97		.338	-61		-612	-97		3-1-4			œ	ç,		169.		305	- 97		-33	- 97	669	. 6.		-668	-91		-115	-97		.668	-97
7.15	565		: -	255		455	-255	;	. 169	-255	1	2772	667.	.754	-255		-770	-255		273	-255		017	255		193	.255	4	608-	667	- 809	-255		3283	-255	308	-255		-826	-255		1418	-255		910	-255
. 82	<u>:</u> :		785	12		228	-12		.207	-12	:		77.	619	-12		129	-12		-113	- 12		.528	13		250	12.		- 266	71.	-338	-12		- 566	-15	283	-12		11	-12		-256	-15		1498	-12
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275	13.		. 351	.54		- 568	- 54	;	685-	\$		1408	ň	124	-54		-266	-54		-332	-54		111	.54		1501	- 54	,	P 2 2	5	-608	.54		-608	.54	125	1.54		-210	,54		-625	.54		- 323	, 54
264	335		827	335		.235	-335	;	- 156	-335	,	- 249	677.	-834	-335		-820	-335		-151	. 335		.131	.335		-529	.335	,	967	crr.	228	-335		-869	-335	. 29.	.335		-210	-335		.257	-335		906-	-335
1870	.7.		.112	.73		.587	.73		. 587	.73	•	7 ;	۲/-	-572	-73		-588	٤٢٠		-588	-73		- 588	-73		-611	-73		179-	2	-627	٤٢-		-627	-73	-644			-644	-73		-644	-73		-644	-73
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. 655	154		1755	-164		125	.164	1	-678	-164	;	-134	101.	-33	-164		-680	-164		-191	164		-249	-164		- 703	-164	,	. 369	501	-512	-164		-719	-164	- 387	-164		-735	-164		1633	-164		177	-164
1167	577		1169	677		398	-611	;	501	-677		-1194		-1176	-677		-1192	-677		-1192	-617		-1192	-617		-1215	-611	:	- 143		-143	-611		207	.611	1.7	-677		-1248	-617		-1248	-677		195	-617
.623	130		-374	-130		928	-130		.145	-130	;	824.	051-	-629	-130		-259	-130		-141	-130		1171	-130		105	-130		200		.195	.130		٤.	-130	ě	.130		932	.130		-198	-130		-128	.130
345	436	٠	312	438	•	94-	438	• ;	9/.	438	• ;	6.4	87.	-61	438	•	.78	438	•	185	438	•	- 78	438	•	.100	438	:	211		.116	438	•	714	438	128	438	•	259	438	•	352	438	• ;	98	438
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ő	585	-87	93	585	-87	7	585	5.1	687	583	- 77	8 6	υ, υ,	173	585	.84	69	585	.75	947	585	.75	69	585	- 83	924	585	90.	15	. 76	. E	585	- 76	31	282	26	585	-77	731	585	-77	820	585	-77	719	585
52	372	4099	120	372	.4102	142	372	-4302	135	372	.4263	.95	3/5	1410	372	.4150	7.1	372	-4305	218	372	.4305	366	372	-4069	9	372		781.	4283	182	372	-4281	408	372	100	372	.4265	-199	372	-4265	-199	372	-4265	199	372
390	. 35	1329	528	- 36	1329	- 550	-36	. 1329	221	-36	-1329	404	97.	.179	.36	-1329	-552	- 36	-1329	. 552	-36	- 1329	.552	-36	-1329	- 86	.36	6761.	1861	1129	223	.36	-1329	233	95-	282	96.	.1329	324	• 36	-1329	.58	-36	-1329	17	-36
																															-351												•			•
699.	178	-4959	-671	.178	-8518	-386	-178	-8572	1507	-178	-8572	231	-178	. 253	178	8539	-694	-178	-8519	1572	-178	-8579	-312	-178	-8579	- 117	-178	7000-	נג	-8669	181	.178	-8669	-194	971-	.171	-178	.8705	.750	.178	-8705	.126	-178	.8705	-169	-178
488	979	7517	487	979	.7518	165	976	-7572	465	979	-7572	462	75.70	480	979	.7539	464	919	.7579	464	919	-7579	164	979	7579	4.11	979	750.	472	7669	425	979	. 1669	425	676	404	979	- 7705	408	919	5066-	408	919	- 7705	408	979
9 []	206	.55	286	206	.12	164	306	7	308	506	7 ;	.311	907	.193	206	12	10	206	Ξ.	310	206	=	.24	205		. 332	205		B + C	-	.133	206	.1	.348	506	145	206	-10	.115	206	-10	.47	206	-10	. 193	206
13.9			130		•	131		:	132		' :	133		134	-		135			136	٠		137			2			27		140			14		142		•	143	•	•	144	٠		145	

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	. 500	. 255		.576	-255		-576	-255		-546	-255		-519	-255		-519	-255		-519	-255		-519	-255		-519	-255		.549	-255		-598	-255		-598	667-	-598	-255		-626	-255		-652	-255		1145	-255		973
	.35	.12		ş	-12		-333	-12		-56	-12		-276	-12		-276	.12		-276	-12		-65	-12		677	-12		214	-12		175	-12		-356	71.	-74	-12		-102	-12		-409	-12		38	-12	į	-378
	29	2.1		. 294	23		-294	27		- 265	27		-237	27		121	27		-237	27		-237	72		.237	22		.267	27		-317	27		-317	*	200	27		364	27		-370	23		-339	27	;	401
	66	 		247	ķ		375	· \$4		70	-54		170	-54		.318	-54		178	.54		80	-54		.318	. 54		466	- 54		-14	-54		.397	, ,	92	-54		354	-54		-36	-54		-156	-54		-420
	G.	. 335		.174	. 335		959 -	-335		-626	-335		=	- 335		- 599	-335		-599	.335		280	-335		.599	-335		-629	-335		- 196	-335		331	c	264	.335		- 706	-335		-732	-335		315	-335	:	268
	419	.73		26	-73		-394	٤٠.		-364	-73		96	-73		-337	-73		.337	-73		-337	-73		-337	٠73		-367	-73		-416	5٠-		342		-416	. 67-		- 444	-73		-470	-73		-439	-73	:	-439
	.305	41		4	4		-280	41		-251	÷		-223	41		-223	7		183	41		-223	41		-223	41		.253	41		279	43		201	4	.303	41		182	4		641	41		583	Ţ	;	-325
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	1022	-617		- 997	-611		.997	-677		686	-677		. 941	-677		-185	-677		- 941	-677		-941	-677		.134	-611		-971	-611		284	-633		808		-1020	-611		-1048	-677		459	-677		-1043	-677	:	-1043
	302	-130		328	-130		149	.130		.174	-130		-139	-130		387	-130		491	.130		233	.130		154	.130		573	-130		160	-130		-298	061-	-474	-130		-502	-130		-527	-130		.97	-130	:	243
•	304	438	•	117	438	•	117	438	٠	146	438	•	174	438	•	405	438	•	386	438	•	174 .	438	•	480	438	•	144	438	•	95	438	•	95	n •	307	438	•	99	438	•	473	438	•	72	438	• ;	240
•	248	635	•	-956	-635	•	-956	- 635	•	-234	-635	•	-899	-635	•	-521	-635	•	668.	.635	•	- 899	-635	•	-818	-635	• ·	-23	-635	•	.316	-635	•	-514	٠,٠	-979	-635	•	-310	.635	•	-434	.635	•	-1001	.635	• :	19
.72	240	585	۲۲.	616	285	- 70	165	585	- 70	293	585	- 70	999	585	-69	321	585	-69	1035	585	-69	731	585	-69	321	585	- 82	291	585	.93	242	585	-71	769	2 -	242	585	-85	1384	585	-84	163	585	.72	1103	585	- 72	946
4368	1.3	3.12	4379	322	372	.4390	208	372	-4390	80	372	.4404	108	372	-4415	108	372	4416	109	372	-4416	380	372	-4416	108	372	4172	78	372	-4008	56	372	-4381	5 6	1000	29	372	-4127	~	372	-4139	-25	372.	-4354	245	372	4369	و
1329	2.8	35	1329	7.7	-36	.1329	. 357	.35	-1329	108	-36	.1329	-300	- 3€	-1329	324	.35	.1329	575	-36	.1329	.300	.36	.1329	.300	36	.1329	.330	-36	-1329	.379	.36	-1329	392	96-11	544	-36	.1329	929	-36	-1329	1140	.36	-1329	234	- 36	-1329	-403
732	865	-352	. 732	-673	.352	. 132	.264	-352	-732	174	-352	. 732	. 616	- 352	. 732	.616	.352	. 732	.616	.352	. 732	32	. 352	-732	-213	-352	-132	-646	.352	-732	-39	-352	-732	7 (לכנ- כננ-	-286	-352	-732	.315	-352	-732	-749	.352	- 732	.718	-352	- 732	-428
. 4275	524	178	-4174	-499	-178	-8019	234	-178	-3902	.165	-178	-3902	714	.178	- 7832	.443	-178	.7832	-443	.178	-7832	.443	.178	-7832	.443	-178	-7832	- 95	.178	-7934	-522	.178	. 80 pl	. 522	1000	391	B.1.	.8091	-373	-178	-8173	-576	-178	-3965	0	178	.8156	.116
7156	634	919	.7095	658	919	-7019	658	979	- 7019	689	919	-6926	1595	979	-6832	1928	979	6832	715	919	. 6832	715	979	-6832	1759	979	.6832	685	919	-6934	636	979	1604	635	1002	1352	979	. 7091	1019	919	.7173	285	979	-7248	613	979	-7156	1190
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-6-		76.	.97	461	.97		812	-97		448	- 97		-480	-97		2 5	À	107	. 97		.454	1.6		45.4	70		855	-97		584	- 97		456	- 6.	211	-9.		147	-97		-478	- 97		-494	-97	
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7.7		.370	27	148	27		372	72		-357	23		.357	27		6 6	•	-323	27	1	341	27		.341	27		-341	27		.355	27		-355	7	- 355	27		-355	27		-355	27		-370	27	
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.335	;	200	- 335	-122	-335		185	-335		620	-335		251	-335		-718	c	-684	-335	:	.279	-335		-13	-335		-214	-335		-74	.335	. ;	330	crr-	206	-335		-716	-335		-292	-335		416	-335	
٤٢٠	;	214	.73	-105	-73		186	-73		-456	-73		-456	-73		-456	?	-422	.7.		10	-73		-440	-73		-440	- 73		202	-73		804	٤/٠	462	.73		402	-73		-454	.7		263	-73	•
÷		.357	.	.357	4		-357	‡		.343	41		-343	41		. 343	;	204	1.5		.327	4		.327	41.		74	41		-341	41		. 341	7	-341	41		-341	43		-341	41	-	-357	41	
-154	;	392	154	69-	-164		429	-164		1,1	-164		307	-164		-548	† C T	-514	-164		-45	-164		-467	-164		-207	-164		73	.164		346	*47	-546	-164		-546	-164		- 59	-164		-561	-164	
577	•	101	119.	.1074	-677		-1074	-677		377	-677		224	-677		377		828	-677		399	-677		320	-617		1203	.677		306	-617	:	. 64		- 97	-617		-1058	-617		-253	-611		-1074	-677	
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438	• :	4 ;	878	380	438	•	382	438	•	487	438	•	240	438	•	167	•	88	438	•	412	438	•	70	438	•	140	438	•	116	438	• ;	716	9 •	228	438	•	364	438	•	663	438	•	487	438	•
- 635	•	-1032	۲, و د	-1032	.635	•.	-1032	.635	•	.493	-635	•	-292	.635	•	98/	•	-887	-635	•	.326	-635	•	-477	-635	•	-186	-635	•	-1017	-635	• !	101.	cro.	-1017	-635	•	-266	-635	•	.362	-635	•	-1032	-635	•
585	.72	90 00	282 - 72	566	585	-72	893	. 585	-72	583	585	-72	202	585	-72	2101		663	585	- 80	218	585	-72	218	585	-72	218	585	- 79	363	585	- 72	2 0	cBc 27.	772	585	-72	204	585	-72	921	585	- 80	666	585	.72
			312																																		•			•			•			•
- 35	1329	55.	-1129	-433	-36	-1329	-433	.36	-1329	-419	- 36	.1329	-419	- 36	1329	619	9241.	- 56	.36	-1329	.403	.35	.1329	-403	- 36	-1329	.403	.36	-1329	-417	-36	-1329	9 4	-1329	-311	.36	-1329	299	- 36	-1329	290	-36	-1329	183	-36	-1329
-352	. 732	5	732	121	.352	.732	- 749	.352	. 732	-376	-352	.732	-215	-352	. 132	181.	.732	156	-352	.732	•36	.352	- 732	-720	-352	.732	.720	-352	-732	204	-352	732	60.	- 732	192	.352	.732	-331	.352	- 732	448	- 352	-732	229	.352	.732
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.652	255		652	522		-626	-255		-652	-255	į	- 652	-255	į	-652	557-	,	700-	667-	,	700	467-	,	652	. 522	ţ	-652	-522	653	-255		- 652	-255		-652	-255	í	256-	;	5	700.	-255	;	269-	467.	Ş	- 652
175	.12		-230	-12		-123	.12		146	-12		۲ :	-12	;	-203	71-			71.	9	50.5	. 12		157	. 12	•	604.	-12	404	.12	!	. 65	-12		7	-12	;	112	:	;	177	-12	;	. 67	71,	;	513
3:0	7.2		3	, 27		.345	72		-310	72		-370	27	;	. 18	7		? ;	7	:	0 5 7 -	7.7	:	146	27	:	346	2	.170	27	i	-18	27		148	27	900	7,0	;		P 1	27	:	289	7	,	- 140
			45.4	55		-425	- 54		Ģ	-54		-63	-54	;	1451	, 54 4	;	ē :		į	142	-54	;	.451	.5.	:	126	-54	.451	. 54		-145	-54		72	-54	:	י פרני	;	3	ň	- 54	;	61.	-54	;	7
601	335		.111	-335		-659	-335		-119	-335		-732	-338	1	-732	-338	:	261-	crr-	;	757	- 335		-732	-335	;	-732	- 335	213	-335		-257	-335		22	-335	í	261-	1	900	505	-335		- 40	- 135	;	361
.470	2	!	-470	-73		29	-73		-470	.73		-470	-73	:	-21	- 73	;	į.	٤/٠		700	• 7.3	•	-470	-73	•	-470	-73	833	- 73	:	-359	-73		260	-73		1022	?		7	-13		-470	. 73		550
22	7	:	.357	41		-331	4		-357	‡		-357	. 41		-357	4			7.5	,	/55.	1	•	6	7	1	-357	41	. 15.7	2	:	-357	43.		-357	7	;		-	6	0	5		-357	4	,	.357
200	154		-561	-164		225	-164		-456	-164		-456	-164		-561	- 164	:	? ;	- 164	į	100.	-164	;	200	-154	;	-561	-164	84	-164		-561	-164		-561	-164	i	154		į	TOC	-164		102	-164	į	-561
1074	67.2		-1074	-677		-1048	-677		-1074	-677		665	-611		-1074	-617		- 101-	-6.1		-107	-617		-1074	-67		-1074	-677	141	.677	•	210	-611		-1074	-633		P/01-		,	200	-677	į	290	-611	;	464
83	-130		340	-130		-182	- 130		-180	-130		-527	-130		169	-130	;	171	051-	į	R :	-130		-527	-130	:	-41	-130	.162	130		-180	-130		-276	-130		107.	1	6	007-	-130		-273	.130	ò	-276
• 626	43.8	٠	718	438	•	748	438	•	375	438	•	434	438	•	378	438	• ;	977	4 7 6	• ;	909	438	•	436	438	• ;	898	438	. 404	4,2	•	297	438	•	574	438	• :	4 4		٠;	7	438	•	6	438	• ;	271
, ,	5.5	•	- 92	-635	٠	.13	-635	•	-1032	-635	•	174	-635	•	396	-635	•	443	619-	• ;	S :	.635	•	-20	-635		212	-635	, ,,	, F. 3.	•	.1032	-635	•	-1032	-635	• ;	-644	•	, ,	976	-635	• ;	-655	-635	• ;	-1032
7.2		27.	188	585	-72	214	585	- 84	186	285	.72	430	585	- 72	188	585	7.1.	188	282	.72	5 1	282	7/	88	\$8\$	27.	188	585	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	282	- 72	1072	585	.72	188	585	7.75	20 2	2 6	77.	9 1	282	-72	186	283	27.	188
1354	37.5	.4354	214	372	-4354	-	372	-4139	514	372	-4354	186	372	-4354	132	372	4324	456	372	-4354	57.	372	-4154	4 9 4	372	-4354	4.	372	PC .	17.	-4354	333	372	-4354	.25	372	.4354	57.	3 .	P C C P C	\$7.	372	4 354	362	372	-4354	365
.1329		.1329	-433	.36	-1329	-407	-36	-1329	-433	.36	-1329	- 80	-36	-1329	-162	-36	-1329	~ ;	9.	-1329	99	- 36	1329	552	-36	1329	203	- 36	6781-	, ,	-1329	338	-36	-1329	112	- 36	.1329	143		6761-		.36	-1329	-433	- 36	-1329	-433
732	34.5	.732	.749	. 352	-732	- 66	-352	-732	522	352	- 732	66	-352	.732	118	.352	-732	473	. 325	- 732	-156	.352	- 735	25	.325	-732	-63	.352	740		. 732	127	. 352	-732	181	-355	. 732	-156	200	26/.	/7-	.352	-732	261	-352	-732	294
308	178	824B	.199	-178	-4226	-121	-178	-8173	-576	-178	8248	.298	-178	.8248	-576	178	-8248	. 576	. 178	8248	-576	.178	-8248	.576	178	8248	.576	-178	8678-	178	8248	-576	-178	-8248	- 576	-178	-8248	976-		9779	9	-178	-8248	- 101	.178	. 8248	925
7248	920	.7248	562	919	7248	60B	979	-7113	1461	616	-7248	1227	616	7248	285	919	. 7248	285	616	.7248	1085	979	-7248	582	919	.7248	1546	979	847/-	070	-7248	1298	616	-7248	993	919	-7248	582		967/-	287	919	-7248	585	979	-7248	285
2 7	300	5 -	191	206	.89	171	206	-15	-191	206	-14	212	206	-14	612	206	-	. 191	506	.14	572	206	-	191	206	7	161	206	4.	9 0	-14	303	206	-14	127	206	7	241	0 .	• •	615	206	-14	127	206	. ·	20
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.652	.255		-652	-255		-638	-255		-638	-255		-638	-255	;	964-		-638	-155		-638	-255		819	255		638	255		638	-255	;	979	557.	-638	-255		-652	-255		-652	-255		-652	.255		-652	- 255
.182	.12		604-	.12		181	-12		-395	.12		-395	-12	į	235	:	-113	-12		-360	-12		195	=		615	22		187	.12	;	- 360	-15	342	-12		309	-12		33	-12		-409	-12		-127	-13
٠ -	12		473	27		462	27		-357	27		162	27	į	909	i	95	27		-357	2.7		104	£.		151	2.3		-	27	;	9 6	,	-283	27		96	23		-13	27		-370	27		-227	27
8.7	\$5.		-451	.54		-137	- 54		. 536	.54		636	-54	;	362	;	-437	-54		458	-54		.22	.54		312	.54		-49	-54	į	2	40	-437	-54		-451	-54		-392	- 54		- 60	-54		-208	-54
17	335		68	-335		-718	-335		-718	-338		121	-335	;	977		-718	-335		-230	-335		434	-335		-374	-335		-105	.335	ì	97.	555	- 84	-335		-628	-335		-732	-335		240	-335		246	-335
97	.73		- 329	٤٢.		277	.73		228	.73		-456	-73		456	•	-456	-73		-456	.73		.456	.73		-456	-73		338	.73	;	d.	۲/۰	72	-73		324	-73		-470	-73		-410	-73		-359	-73
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195	191		46	-164		364	-164		362	-164		-548	-164	;	164		90	-164		-119	-164		-548	-164		-224	-164		269	-164		405	* OT -	-548	-164		-238	-164		343	-164		93	-164		-489	-164
0	577		.1074	.617		-843	-677		-1060	677		418	-677		-1060	•	11	-617		-398	-617		-1060	-677		-1060	-617		-1060	-677	;	262		-1060	-617		-1074	-611		-1074	-611		- 926	-677		-1014	-677
	.130		370	-130		-104	-130		-233	-130		-513	-130	,	997-		-513	-130		-338	-130		-513	-130		-259	-130		-513	-130	í	515	7.7	-140	-130		-30	-130		~	.130		139	.130		184	-130
305	438	•	94	438	•	188	438	•	407	438	•	22	438	• ;	V 4		450	438	•	420	438	•	240	438	•	286	438	•	316	438	٠ ;	- :	*	538	438	•	159	438	•	638	438	٠	271	438	•	521	438
6.53	.6.15	•	.245	.635	•	.193	.635	•	-1019	-635	•	- 1019	-635	• ;	247.	•	-113	.635	•	-202	-635	•	-162	-635	•	. 264	-635	•	.314	-635	• :		000	. 555	-635	•	-655	-635	•	112	-635	•	238	-635	•	- 655	635
e.	585	.72	188	582	-72	202	585	. 72	202	585	. 72	1009	282	27.	7 2 2	-72	202	585	-72	762	585	-72	1012	285	. 72	656	585	- 72	202	585	. 72	10/8	-72	202	585	.79	188	585	- 72	188	585	-72	188	585	- 72	188	585
۶.	22	-4354	.25	372	-4354		372	-4362	Ξ.	372	-4362	231	372	-4362	11.	-4362	228	372	-4362	Ξ.	372	-4362	-11	372	-4362	200	372	-4362	-11	372	-4362	1 :	-4352	122	372	-4228	- 25	372	-4354	144	372	-4354	-25	372	-4354	-25	372
ĩ	. 35	.1329	337	-36	.1329	-419	-36	.1329	.91	-36	-1329	217	.36	-1329	414	-1329	-419	-36	-1329	289	-36	.1329	197	- 36	-1329	68	-36	-1329	-419	-36	1329	757	1329	982	.36	.1329	24	-36	-1329	-433	.36	-1329	-433	.36	.1329	487	-36
-	352	-732	.341	.352	. 132	-735	.352	732	183	-352	. 132	.221	-352	- 732	667.	732	151	- 352	-732	.215	.352	-732	-212	.352	-732	.735	-352	.732	-376	.352	-732	517	732	.610	.352	-732	302	.352	-732	.391	- 352	.732	-23	.352	.732	304	-352
346	1:8	8248	163	-178	.5048	-24	.178	.8210	. 562	-178	-8210	. 552	. 178	0128-	2¢ 871.	8210	692	-178	.8210	245	-178	-8210	202	.178	.A210	-86	.178	-8210	62	-178	.8210	, r	.8210	-257	.178	.8210	-489	-178	.8248	.576	-178	.8248	102	-178	-6248	148	.178
5.8.2	616	.7248	282	616	. 7248	296	916	-7210	1688	979	-7210	1100	979	017/-	979	7210	1484	616	-7210	1326	979	. 7210	296	979	7210	965	979	.7210	296	979	.7210	9 6	.7210	296	979	-7210	\$82	979	-7248	285	919	-7248	282	979	-7248	285	979
191	206	+1.	9	206	. 54	. 82	506		-177	206	- 13	403	206	57-	706	.15	143	206	.15	143	206	-15	189	502	-15	399	206	12	.117	206	51-	146	-15	559	206	-15	נרנ	506	-14	286	206	-14	393	506	- 14	321	206
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										384	>			-45	.12		-84	-12		344	.12		271	.12		.367	-12		- 363	-12		399	-12		-367	-12		-367	-13		70	-12		•	-12		-385
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										45	œ			-652	-335		- 266	-335		-690	.335		969	-335		619	-335		-690	-335		-690	.335		9	.335		-41	-335		-690	-335		- 708	-335		357
										-313	0			.390	.73		-428	.73		-63	- 73		-63	-73		-428	-73		-428	-73		-428	-73		-88	.73		22	-73		363	-73		-446	.73		487
										-21	D.			132	41		544	41		206	4		-315	7		-315	41		267	41		999	4		80	41		-315	41		270	41		461	41		178
										-142	2			223	-164		458	-164		-520	.164		.520	-164		1055	- 164		384	-164		-520	-164		.124	- 164		1118	-164		726	-164		- 16	-164		-538
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										902	د			66	-130		-486	-130		- 75	-130		16	-130		.310	-130		-486	.130		-486	-130		-486	.130		.310	-130		-205	-130		300	-130		-39
										249	¥	ė,		121	438	•	424	438	•	83	438	•	83	438	•	83	438	•	83	438	•	344	433	•	83	438	•	83	438	•	718	438	•	277	438	•	457
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					Plan9		666	-1000		338	·H	Ĭ. *		.154	.352	.732	.707	-352	.732	-707	.352	-732	. 111	.352	.732	-153	. 352	.732	-187	.352	. 732	.707	.352	-732	. 107	.352	-732	- 59	-352	-732	.707	-352	-732	-725	-352	-732	161
					olo ne e		8 11:46:04 1999	-1000		85	0	ρ́	68.	-495	.178	-8015	-534	.178	-8128	.534	.178	-8128	.534	-178	.8128	-534	-178	-8128	-111	.178	.8128	534	178	-8128	-534	-178	.8128	-158	-178	-8128	.111	.178	.8128	. 552	-178	-8180	-552
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-44	27		-44	27		-44	27		-44	•	
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-422	-352	-732	-422	-355	-732	-422	-352	-732	-422	•	٠
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	-1998 W	-325	-325	-325	-325 -255 -325	.325	-325 -255 -325 -325	-325
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	-21 P	-30	-30	41	-30	41	-30 41 961	-30
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- 865	-255		-814	-255		555	-255		-1992 -	-255		-2464	-255		-6824	-255		- 6203	-255			-255			-255		-1262	-255			-255		- 3636	-255		-1243	-255		-3539	•	
-1448	-12		-1299	-12		-1400	-12		-1581			-1239	-12		•	-12		-1001	-12		ņ	-12		-209	-12			-12		-777	-12		-1339	-12		159	-12		-3296	•	
-748	27		495	27		246	27		-584	27		157	27		511	27		-678	27		888	. 27		-295	27		51	27	•	137	27		688	27		1466	27		-3257	•	
127	, S4		1526	.54		864	-54		1444	-54		1940	-54		487	-54		-674	-54		-651	-54		-1072	-54		-1820	-54		-1684	-54		-1589	-54		-1006	-54		-3338	•	
569	-335		1141	-338		832	-335		1033	-335		- 95	-338		233	-335		723	-335		873	-335		1467	-335		1062	-335		1360	-335		2450	-335		-1729	-335		2073	*	
508	-73		-38	-73		1920	-73		330	-73		-230	-73		994	73		-79	-73		1062	-73		1387	-73		684	-73		2189	-73		-1564	-73		-1357	-73		-3357	*	
-2694	41		-2307	41		-2630	41		-1477	41		-2358	47		-3697	41		-4263	41		-3424	47		-4183	41		-3370	41		-5237	41		-5143	41		-4231	41		-3243	•	
-577	-164		178	-164		-331	-164		535	-164		-306	-164		860	-164		-1273	-164		-261	-164		- 942	-164		-2273	-164		-1849	-164		-2678	-164		-3164	-164		-3448	•	
-2434	-677		-475	-677		-1174	-677		1102	677		- 963	-677		-2243	-677		-1515	-677		-630	-617		222	-677		66	-611		837	-677		-177	-677		-135	-677		-490	•	
-1688	-130		-352	-130		-772	-130		313	-130		573	-130		301	-130		2042	-130		-985	-130		-447	-130		-1530	-130		-1048	-130		-2701	-130		-1812	-130		-3414	•	
126	438	•	322	438	•	-178	438	•	803	438	•	-777	438	•	56	438	•	-391	438	•	238	438	•	915	438	•	-144	438	•	207	438	•	587	438	•	-674	438	•	-615	*	D
-1502	-635	•	119	-635	•	-287	-635	•	-707	-635	•	-470	-635	•	-152	-635	•	-855	-635		1003	-635	•	-112	-635	•	-140	-635	٠	377	-635	•	781	-635	•	202	-635	•	-208	•	•
2289	585	٥,	1817	585	9	2532	585	- 7	2297	585	ç	2555	582	4.	2735	585	۲-	2931	585	α γ	3101	585	4	3324	585	4-	4399	582	ŗ.	3105	582	÷	3678	585	5,	3848	585	-2	4734	•	•
-2298	372	-7375	-1006	372	-7964	-2012	372	-7645	-1572	372	-8190	-1671	372.	-8347	-1706	372	-7610	-3338	372	-7551	-2686	372	-8538	-2648	372	-8629	-3390	372	-8760	-3135	372	-8841	-3908	372	-8708	-3284	372	-9456	-2912	•	•
3123	- 36	-1329	-1287	-36	-1329	-581	-36	-1329	-914	-36	-1329	-1088	-36	-1329	-751	-36	-1329	-530	-36	-1329	-1857	-36	-1329	-2200	-36	-1329	-3104	-36	-1329	-3026	-36	-1329	-3127	-36	-1329	-3424	-36	-1329	-3320	•	•
-2264	-352	-732	-1979	-352	-732	-1479	-352	-732	-1992	-352	-732	-1433	-352	-732	-1553	-352	-732	-1630	-352	-732	-1478	-352	-732	-809	-352	-732	-2768	-352	-732	- 940	-352	-732	-3827	-352	-732	-3938	-352	-732	-3636	•	•
-2180	-178	-4171	-2078	-178	-6030	-1100	-178	-4065	-1983	-178	-3931	-1189	-178	-4347	-812	-178	-4124	-2516	-178	-4507	-2380	-178	-5598	-2842	-178	-3370	-3708	-178	-3975	-5317	-178	-2455	-4863	-178	-1998	-4411	-178	-1501	-3462	•	•
-1425	979	-15392	-163	616	-15295	-67	919.	-15269	- 767	979	-15160	-1977	979	-15033	-1100	979	-14935	-1759	919	-14816	-1028	979	-14726	-1394	979	-14683	-1950	979	-14454	-1108	919	-14302	-2107	979	-13813	-2243	979	-13206	-2305	•	•
-1118	206	-82	-695	206	-22	-1656	206	-83	-1399	206	- 98	-1156	206	-73	-838	206	-85	-1917	206	-65	-826	206	.30	-1830	206	147	-3489	206	-95	-2572	206	-290	-2039	206	-416	-2699	206	-629	-3078	•	•
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	-1998	3:		-2704	- 255	-2252	-255		-1118	- 255		-2273	-255		-2307	552-	-2409	-255		-1783	-255		-2572	-255		-1662		
	384 -	>		-2035	-12	.1221	-15		-1358	-12		-1286	-13		-1243	-15	-2118	-12		-1093	-12		-1120	-13			-12	
	201	H		-794	27	64	27			27		-79	27			1.7	-1097	27			72		-565	27		334	27	
	531	vs		480	5.	208	- 54		-39	-54		1008	-54			44-	-82	-54		-326	-54		-193	-54		1021	-54	
	45	æ		-1338	- 335	-420	-335		-1003	-335		-357	-335		-175	445	-389	-335		689	-335		672	-335		256	-335	
	-313	o		-637	- 73	610	.73		-151	.73		217	-73		384	٢/٠	419	.73		231	-73		-982	-73		355	-73	
				- 5309	41	-1185	41		-4147	41		-1203	41		-4319	4.1	-3558	41		-2666	41		-3204	41		-2509	41	
	-142	z	•		-164	-382	-164			-164			-164			-164	-1428				-164		- 905	-164		-1030		
	-1085	Σ		-2350	-677	-1982	-677			-677		-1778	-677			1/9-	-2151				-677		-1441	-677		-1594		
		.1			-130	-252	-130			-130			-130			061-	-840				-130		- 947	-130			-130	
	249	× ,		-295	4. E. 4	1212	438	•	352	438	•	754	438	• ;	735	# *	935	438	*		438	•	2484	438	•			
	-4 197	₩	Ĭ.	-1725	-635	-1168	-635	•	-788	-635	•	-1097	-635	•	-1198	٠ ٠	-942	-635	٠	-878	-635	•	-178	-635	*	-516	-635	•
•	-8455	≈ 7	3	1673	-331	636	585	-438	375	585	4.	851	585	65.	2152	282	1732	585	-17	1259	585	-16	1740	585	-26	362B	585	9,
	-4	ئ ئ	j.	-1682	3/2	-323	372	-1934	-1723	372	-5068	188	372	-5215	328	2/5	- 59	372	-6404	2061	372	-6487	-2173	372	-5831	-473	372	.7321
. IMM	-8455	E		1700	-36	-22	-36	-1329	-414	- 36	-1329	-2137	-36	-1329	265	-1129	-869	-36	1329	737	-36	1329	1300	-36	1329	781	-36	. 1329
Plan9 HMM	338	Э .		-1340	-352	1115	-352	-732	156	-352	-732	626	-352	- 132	1680	- 732	-2041	-352	- 732	-770	-352	- 732	-2139	-352	- 732	-2169	-352	-732
0	-1000 85	O /	-2550	-1674	-178	-1301	.178	-9267	-1636	-178	-7638	-528	-178	979/-	-336	-6520	-2740	-178	-6415	-725	-178	-5811	-3207	-178	-5582	-1939	-178	-3683
E S.	-8455 -1558	υ ; , į	•	3160	919	2346	979	-15573	4599	919	-15622	2689	979	/1991-	1612	-15614	4373	979	-15598	103	_	-15581		979	-15554	1020	979	-15524
MAMER2.0 MAME ikaros-mus.txt DESC LENG 23 ALPH Amino RF no CG no CG LCOM , [converted from an NSEQ 0 DATE MON MAR 8 11:45:3:	-8455 -4 - 595 -	4 ×	-270	-1764		-957			-2152			- 720			//91-			206	-17	-710		- 56	-1181	206	-30	836	206	-111
ER2 EG # G E	XT NULT NULE	нмм		н .		7			٣			4		, .	n		9	•	•	7	٠	•	85	ı	•	σ,	•	•
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-617	-97		.483	-97		-432	-97		-378	•	
-775	- 255		-641	-255		- 590	-255		-537	*	
	-12			-12		-348	-12		-294	•	
	27		-160	27			27		1973	•	
942	-54		879	- 54		1646	-54		-336	•	
-855	-335		-444	-335		0.29-	-335		-617	•	
-593	-73		-459	-73		-408	-73		-355	•	
-480	41		-345	41		- 295	41		-241	•	
-684	-164		-36	-164		-500	-164		-446	•	
-1197	-677		-1063	-677		-1012	-677		-958	•	
	-130										
378	438	٠	22	438	٠	102	438	•	156	•	0
-1155	-635	•	-1021	-635	٠	-971	-635	•	-917	•	٠
	585										•
-148	372	-4478	-14	372	-4535	36	372	-4604	90	•	٠
-556	-36	-1329	-422	-36	-1329	.372	-36	-1329.	-318	•	٠
.872	-352	- 732	- 305	.352	-732	-688	-352	-732	-634	•	•
669,	-178	-2089	1278	-178	-2998	-514	-178	-3348	-460	٠	•
459	919	-6982	593	919	-6474	644	616	-6305	697	•	•
-314	206	-402	-180	206	-212	381	206	-170	- 16	٠	•
72			73		٠	74	,	•	75		,

	-1099	-97		-61	-97		78	-97		-13	-97		.951	-97		-951	- 97		-951	-97		-907	- 97		-907	-97		-894	-97		1279	- 64		-743	-97		-712	-97		- 706	.97		-682	-97	
	-1257	-255		-1257	-255		867	-255		-314	-255		-1110	-255		-1110	-255		2591	-255		681	-255		404	-255		-1052	-255		2283	-255		-901	-255		-870	-255		-864	-255		3347	-255	
	47	-13		-834	-12		-344	-12		859	-12		-55	-12	•	-502	-12		-69-	-12		1473	-12		- 94	.12		1020	-12		95	-12		1847	-12		-628	-12		79	-12		115	-12	
	623	27		412	27		18	27		368	27		933	27		-528	27		1097	27		160	27		1536	27		-195	27		936	27		-129	27		-360	27		-583	27		823	27	
	533	-54		137	-54		-184	-54		-947	-54		- 909	- 54		-52	- 54		-480	- 54		.864	.54		-273	.54		508	-54		-239	-54		-372	- 54		-178	- 54		561	-54		100	-54	
	-1337	-335		-1337	-335		-1228	-335		-418	-335		- 929	-335		-1190	-335		-1190	-335		-1145	-335		-1145	-335		-1132	-335		-838	-335		-199	-335		903	-335		-944	-335		- 70	-335	•
	1183	-73		-188	-73		619	-73		-282	٠٦3		2454	- 73		592	-73		-355	57.		-883	.73		106	-73		-870	-73		-844	- 73			-73		1998	-73		118	- 73		-658	-73	
	- 962	41		-962	41		926	41		32	41		171	41		-814	41		828	41		-770	41		893	41		262	41		1798	41		24	41		-575	41		-569	41		- 544	41	
	-1166	-164		-1166	-164		-1058	-164		-1058	-164		-1019	-164		-1019	-164		-1019	-164		- 975	-164		746	-164		-961	-164		-935	-164		-810	-164		- 780	-164		-774	-164		-749	-164	
	-1679	-677		494	-677		-1570	-677		-1570	-677		88	-677		-1531	-677		-1531	-677		-1487	-677		-1487	-677		-1473	. 611		-1447	-677		-1323	-677		-1292	-677		-655	-677		-1262	-617	
	-421	-130		1166	-130		-328	-130		265	-130		-636	-130		1400	-130		-617	-130		-657	-130		-488	-130		143	-130		069-	-130		514	-130		-182	-130		1016	-130		-583	-130	
•	1796	438	•	427	438	•	-456	438	•	779	438	•	-417	438	•	755	438	*	-49	438	•	1707	438	•	99	438	٠	-359	438	•	-333	438	•	-208	438	•	-178	438	*	287	438	•	-7	438	•
٠	-1637	-635	•	.1637	-635	•	-1529	-635	•	-1529	-635	•	-919	-635	•	-448	-635	٠	-311	-635	•	966-	-635	•	-1446	-635	•	-1432	-635	•	-1406	-635	•	-778	-635	•	-431	-635	•	869	-635	*	-392	-635	٠
-116	-417	585	-116	-417	585	-116	-308	585	-106	-308	585	-106	-270	585	-102	270	585	-102	-270	585	-102	-225	585	96.	-225	585	- 96	-212	585	.93	-186	585	-91	-61	585	-84	-30	585	- 78	-24	585	-77	0	585	-74
-3696	-630	372	-3696	-630	372	-3696	-521	372	-3825	-521	372	-3825	-483	372	-3876	-483	372	-3876	- 50	372	-3876	-438	372	-3960	-235	372	-3960	-425	372	-3996	-399	372	-4034	-274	372	-4148	-243	372	-4251	-237	372	-4274	-213	372	-4319
-1329	695	-36	-1329	-382	-36	-1329	1741	-36	-1329	-659	-36	-1329	-891	-36	-1329	-891	-36	-1329	-891	-36	-1329	-846	-36	-1329	-846	-36	-1329	-833	-36	-1329	-807	-36	-1329	-682	-36	-1329	159	-36	-1329	-645	-36	-1329	-621	-36	-1329
- 732	-1354	-352	-732	-1354	-352	-732	-1246	-352	-732	-1246	-352	-732	-1207	-352	-732	-1207	-352	- 732	-1207	-352	-732	-1163	-352	-732	-1163	-352	-732	-1149	-352	- 732	-1123	-352	- 732	- 998	-352	-732	-564	-352	- 732	-961	-325	-732	-937	-352	-732
- 9205	-1181	-178	-9205	-187	-178	-2913	-1072	-178	-8972	-1072	-178	-4185	-1033	-178	-8883	-1033	-178	-8883	-1033	-178	-3915	- 989	-178	-8775	-989	-178	-5378	-363	-178	-4564	-949	.178	-2545	-825	-178	-3997	448	-178	-5973	-788	-178	-4279	-764	-178	-2960
-8205	-23	979	-8205	2846	979	-8205	1662	979	-7972	3161	979	-7972	1019	979	-7883	2054	979	- 7883	125	979	- 7883	2183	979	-7775	1556	979	. 1775	3140	979	-7738	1100	979	.7670	333	979	-7341	364	616	-7251	370	979	-7235	394	979	-7154
7.	-143	206	۲.	- 196	206	-211	482	206	ď,	-688	206	-88	461	206	6-	46	206	6-	1236	206	-106	-195	206	-10	-605	206	-42	-101	206	-69	-565	206	-280	-440	506	-103	-410	206	-33	-403	506	-86	-379	506	-210
•	57	•		28	,	•	0,		•	9	•	•	61		•	29			63		ı	64	•	•	65		١	99			67			68			69	,		70		•	1,	,	

-97		-1299	-97		-1299	- 97		57	-97		176	-97		-1207	-97		1045	-97		-1148	-97		744	-97		253	. 97		1994	-97		212	16-		-1128	-97		-1099	-97		-1099	-97		-1099	-97
-255		. 13	-255		-1457	-255		1193	-255		-1387	-255		1973	-255		1487	-255		1824	-255		1484	-255		240	-255		-1360	-255		-1321	-755		-1286	-255		1278	-255		-1257	-255		1184	-255
-12		317	-12		697	-12		392	-12		226	-12		-34	-12		1642	-12		-67	-12		-205	-12		-315	-12		-297	-12		1,74	-15		-259	-12		-834	-12		-185	-12		504	-12
27		427	27		2009	27		1001	27		-73	27		615	27		-121	27		1402	27		832	27		1686	27		297	27		-157	2.1		469	27		-339	27		-976	27		-81	27
-54		1041	- 54		184	- 54		-1221	-54		202	-54		1749	-54		91	-54		674	-54		298	-54		267	-54		566	-54		1252	-54		-579	-54		25	-54		-1056	-54		-1056	-54
-335		-1537	-335		-196	-335		-1502	-335		-1467	-335		-1445	-335		-1425	-335		-1387	-335		-1504	-335		-1472	-335		-1440	-335		-1401	-332		-1366	-335		-1337	-335		-1337	-335		-1337	-335
٠٦3		-21	-73		-1275	-73		666	-73		1109	-73		603	-73		37	-73		-1124	-73		-398	-73		-519	-73		-1178	-73		64	-73		1591	-73		619	-73		129	-73		-1075	-73
7		567	41		14	41		-168	41		-89	41		-475	4.1		-586	41		-787	4.1		438	41		-119	41		1128	41		212	4		1460	41		323	41		-269	41		-405	41
.164		-1367	-164		-1367	-164		-523	-164		-634	-164		-1275	-164		-1255	-164		377	-164		-614	-164		126	-164		-1270	-164		547	-164		-1196	-164		550	-164		-519	-164		1636	-164
176-		893	-677		116	-677		-1844	-677		-1809	-617		-1787	-677		-1767	-677		192	-617		-1846	-617		-1813	-677		-325	-677		-1743	-611		-1708	-677		827	-677		-1679	-677		1182	-677
.130		-1333	-130		-351	-130		946	-130		161	-130		415	-130		252	-130		-123	-130		-645	-130		173	-130		249	-130		-537	-130		264	-130		1160	-130		1518	-130		-182	-130
438	•	368	438	•	-765	438	•	15	438	•	1501	438	•	28	438	٠	4	438	•	732	438	•	954	438	•	87	438	•	20	438	•	-158	438	•	1021	438	•	-564	438	•	539	438	•	1186	438
-635	•	-1838	-635	•	-1838	-635	•	-1802	-635	•	-1768	-635	•	-1746	-635	٠	-1726	-635	٠.	-1687	-635	٠	-1805	-635	*	-1772	-635	•	-1741	-635	•	1701	-635	•	-1371	-635	•	.1637	-635	•	-1057	-635	•	-1637	-635
585	-202	-617	585	-202	-617	585	-205	-582	585	-187	-547	585	-241	-525	585	-226	-505	585	-169	-467	585	-399	-584	585	-200	-552	585	-184	-520	585	-170	-481	585	-143	-446	585	-135	-417	585	-116	-417	585	-116	-417	585
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-36	-1329	-111	-36	-1329	423	- 36	-1329	-119	-36	-1329	-1168	-36	-1329	-1146	-36	-1329	-297	-36	-1329	-415	-36	-1329	-1205	-36	-1329	-1173	-36	-1329	912	-36	-1329	-380	-36	-1329	86	-36	-1329	-1038	-36	-1329	908	-36	-1329	-1038	-36
-352	. 732	.835	-352	-732	-1555	-352	-732	-1519	-352	- 732	-283	-352	-732	-1463	-352	.732	-990	-352	-732	-1404	-352	-732	-1521	-352	-732	-1489	-352	-732	-1458	-352	- 732	-711	-355	-732	- 963	-352	-732	- 923	-352	-732	-1354	-352	-732	-1354	.352
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-327	-36	-1329	879	-36	-1329	657	-36	-1329	159	-36	-1329	442	-36	-1329	722	-36	-1329	749	-36	-1329	61	-36	-1329	2315	-36	-1329	512	-36	-1329	-108	-36	-1329	640	-36	-1329	1691	- 36	-1329	-423	-36	-1329	-1238	-36	-1329	-1238
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372					-																											•			'			•							
-36				_																												305					•						•	96	
-352	- 732 -	559	-352	- 732 -																												-305		•			•			•				452	.352
_			-178	-11431				-2506	-178	11439	-398		5207						_			-11408		-178									_			_	m		-178	_	194	-178	-11401	672	-178
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1447	-12		461	-12	1	,		71.		767	-12		243	-12		83	-12	,	7.7	.12	;	- 166	- 12	,	1927 -	-12	ľ	ָה היי	71.		-424	71-	9	4 C	71-	,	-1989	-12		-2330	-12	***	*CDT-	71-	8	
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-2658	-335		-654	.335	1		2011	- 335	;	334	-335		806	-335		-51	-335		894	-335		606	-335		1334	-335	;	1269	-335		1991	-335	•	481	-335	;	937	-335		833	-335	;	1 4 1	-335	000	200
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-2487	-164		- 914	776	* 0 7 -		1867-	-164		-1020	-164		-1138	-164		-444	-164		-919	-164		-1857	-164		305	-164		- 74	-164		-2319	-164		236	-164		246	-164		730	-164		1016	-164		799
-1553	-677	•	703	700			1282	-677		-330	-677		-2984	-677		166	-677		756	-677		-769	-677		1483	-677		445	-677		-579	-677		-652	-677		1082	-677		226	-677	-	177	-677	- 6	8867-
-240	-130	1	707	00,	130	:	-815	-130		-759	-130		396	-130	-	374	-130		-208	-130		835	-130		165	-130		- 76	-130		406	-130		200	-130		104	-130		631	-130		343	-130		-125
818	8.78	•	26.3	0 0	438	• !	802	438	•	1559	438	•	1015	438	*	961	438	•	1049	438	•	730	438	•	117	438	•	882	438	•	1559	438	٠.	410	438	•	1207	438	•	872	438	•	808	438	• ;	380
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-1679	200	2 6	0 0	96/T-	585	-88	-887	582	-159	-1750	582	-89	-1722	585	-221	-1753	585	- 90	-1743	585	-154	-1733	585	- 93	-1764	585	- 90	-265	585	-89	-1757	585	-159	-1786	585	- 93	-1733	585	-86	1793	582	-86	-1726	585	-82	492
.1951		710	.4065	-1951	372	-4085	-1951	372	-3258	-1963	372	-4061	-417	372	-2814	80	372	-4046	-811	372	-3303	.166	372	-4009	-1977	372	-4041	-126	372	-4067	-694	372	-3262	-1508	372	-4005	-390	372	-4111	-345	372	-4111	431	372	-4129	-471
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777	*****	ου Σ	-10434 -	-1344	979	-10434 -	-1304	919	-10434	533	979	-10449	-1328	979	-10416	-1359	979	10453	-1349	979		-1378	979	-10475	-1370	919	-10466	1243	979		-1362	919	-10457 -	-1392	979	-10492	-539	979	-10429	-1339	979	-10429	-1332	979	-10420	55
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į	168	- 164	0	90	-164		4	-164		-774	-164		64	-164		-1344	-164		268	-164		944	-164		119	-164		820	-164		602	-164		- 48	-164		-2511	-164		-199	-164		-325	-164	
	-3171	-677		-3171	-677		-3171	-677		-1720	-617		1103	-677		-3207	-677		-3207	-677		-299	-677		1591	-677		404	-677		1144	-677		-254	-677		1001	-677		-3058	-677		-377	-677	
;	-332	-130		156	-130		284	-130		759	-130		671	-130		810	-130		815	-130		205	-130		-254	-130		214	-130		-1027	-130	•	-1517	-130	:	-1142	-130		-813	-130		-456	-130	
•	312	438	• (726	438	•	33	438	•	-341	438	•	-135	438	•	454	438	•	929	438	•	221	438	•	-188	438	•	-824	438		179	438	*	-241	438	•	1002	438	•	-1752	438	•	-353	438	•
•	198	-635	• :	-3130	-635	•	-312	-635	•	-170	-635	•	1085	-635	•	103	-635	•	-298	-635	*	705	-635	*	41	-635	•	328	-635	•	1180	-635	•	1526	-635	•	1223	-635	•	780	-635	•	1139	-635	*
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-732	-2847	-352	-732	-1883	-352	-732	-166	-352	-732	-2847	-352	-732	-1335	-352	- 732	-523	-355	-732	-1232	-352	-732	-2827	-352	-732	-303	-352	-732	-1228	-352	-732	-223	-352	-732	-541	-352	-732	-2765	-352	-732	170	-352	-732	-234	-352	-732
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	-1516	979	_	-1516	979	-10639 -	-1516			-1516						-1551	979	•							-1495						618		-10615				-348		-10542				-1403	_	-10505
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. 97		-2597	-97		-2597	-97		-2597	-97		-2519	- 97		-2492	-97		-187	-97		-2555	-97		952	-97		109	-97		-2519	-97		-280	7	982	-97		-391	-97		-2627	-97		101	-97
-255		-2755	-255		-2755	-255		-2755	-255		-2678	-255		-2650	-255		-2713	- 255		-2713	-255		-2713	-255		-2739	-255		-2678	-255		-2678	-255	ac3c-	-255		-2678	-255		-2785	-255		-699	-255
-12		986	-12		-198	-12		671	-12		356	-12		503	-12		-217	-12		817	-12		432	-12		1655	-12		407	-15		-126	71-	225	-12		494	12		1014	-12		166	-12
27		-2474	27		-884	27		-2474	27		-2396	27		363	27		-1719	27		-171	27		- 734	27		136	27		÷	27		-1048	7	75.	27		-265	27		-121	27		709	27
- 54		-2555	- 54		-2481	-54		-506	-54		-983	-54		-2130	-54		153	-54		-1310	-54		.1133	- 54		-2538	-54		-2477	-54		-1523	4.	1461	-54		887	-54		-557	-54		-1180	-54
-335		483	-335		777	-335		-2836	-335		451	-335		-1365	-335		18	-335		96•	-335		- 701	-335		-411	-335		-1111	-335		-2758	-335	Ę	-335		-336	-335		-968	-335		-1021	-335
-73		2236	-73		404	-73		1609	-73		1184	-73		387			868	-73		1353	-73		-1361	-73		-2557	-73		63	-73		-2496	-73	900	.73		-2496	-73		832	-73		-370	-73
41		-819	41		463	41		-548	41		-593	41		-2355	41		-2417	41		- 789	41			41		-954	41		734	41			41	,,,	41	!	-705	41		361	41		1057	41
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-677		-3177	-677		-93	-677		-3177	-677			-677		-3072	-677		-3134	-677		-2998	-677		618	-611		-1690	-677		1232	-617		-3099	-677	1774	-677		-3099	-677		-323	-677		-3207	-677
-130		-1358	-130		383	-130		594	-130		-285	-130		995	-130		843	-130		456	-130		307	-130		-125	-130		489	-130		621	-130	. 5	-130		324	-130		999-	-130		15	-130
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-635	٠	281	-635	•	96	-635	•	249	-635	•	740	-635	•	266	-635	•	-342	-635	•	986	-635	•	577	-635	•	1138	-635	•	473	-635	•	195	-632	• 0	-635	•	297	-635	•	1196	-635.	•	396	-635
585	-121	-1004	585	-121	194	585	-121	649	585	-383	1674	585	-105	-254	582	-270	181	585	-111	438	585	-111	1034	585	-195	1405	585	-118	898	585	-105	380	585	-105	7.87	-105	-1838	585	-443	85	585	-131	721	585
372	-3641	-2129	372	-3641	-1566	372	-3641	-1332	372	-2102	-1036	372	-3836	4	372	-2549	-125	372	-3752	009	372	-3752	-58	372	-2984	-1584	372	-3669	-504	372	-3836	-1279	372	-3836	372	-3836	-2051	372	-1919	-537	372	-3521	-981	372
-36	-1329	517	-36	-1329	-2433	-36	-1329	-2537	-36	-1329	-282	-36	-1329	-2431	-36	-1329	-2494	-36	-1329	-317	-36	-1329	34	-36	-1329	-2520	-36	-1329	9	-36	-1329	-585	-36	-1329	7/5	-1329	-733	-36	-1329	940	-36	-1329	-2566	- 36
-352	-732	-214	-352	-732	. 809	-352	-732	-668	-352	-732	-806	-352	-732	-1158	-352	-732	-1630	-352	-732					-352	-732	-2836	-352	-732	-355	-352	-732	-1111	-352	-732	-352	-732	-1165	-352	-732	-1656	-352	-732	-1242	-352
-178		579	-178	11646	-231	-178	11646	1019	-178	-3066	-188	-178	•		m			-178	-11596	338	-178	-11596		_			-178	_		_	_		_	11554	. ~					_	-178	11681	488	-178
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	3	27		-383	27		-285	27		-1007	24		.578	27		-138	27		28	27		1096	27		-166	27		754	27		40	27		-140	27		653	27		-202	33		-831
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	423	-164		1051	-164		613	-164		748	-127		1775	-164		595	-164		1279	-164		-121	-164		412	-164		619	-164		149	-164		-12	-164		- 909	-164		-1607	-175		-1191
	-2433	-677		-1627	£49- ·		-1708	-617		-1943	-688		-2729	677		-3041	-677		-2061	-677		-3184	-617		-2256	-677		-2017	-677		-1935	-677		-1414	-677		-1406	-677		-1811	-690		-2708
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-220	126	585	-115	936	585	-51	-254	585	-101	134	597	φ,	277	585	-29	903	585	-15	-150	585	-11	- 760	585	-32	-819	585	-36	340	582	-41	-916	585	-20	-15	585	-15	-162	585	-11	-388	579	'n	-1228
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3250	979	-15462	4437	1117	٠,	4555	979	-15759	3284	979	-15772	3432	979	-15769	3058	. 979	-15775	2474	979	15771	3045	919	15769	3160	979	15758	2996	979	15750	3206	979	15771	3474	979	15771	3029	979	15758	4079	979	15750	3192	979
-1122	206	-112	-1556	183	9906-	-1832	206	ŗ	-1081	206	-13	-891	506	-10	-1191	206	-12	-982	206	-11	-1194	506	- 54	-1739	506	- 55	-1505	206	-15 -	-1466	206	2	-1490	506	-23	-1375	506	- 22 -	-1754	506	-33	-432	206
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	384	-860	-12	-615		-1185	-1609	-12	-1083	-12	-260	-12	.772	4		-1151	-13	-444	-12
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	531 S	-440	-54	-631	į	- 394	-346	-54	-369	-54	-299	-54	1861	-57		-429	-55	-612	- 54
	2. g.	-496	- 335	-1066		-335	. 56	-335	-1204	-335	259	-335	.640	-337		-1273	-328	-763	-335
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	902 L	-1082	-130	-1201		-1856	-1312	-130	-2058	-130	-1515	-130	1602	-150		-1748	-147	-1860	061
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- 8455	-1158 H d·->d	-224	-406	-179 595	-268	1204 585	-218	585	-549	585	380	585	-373	579	-265	186	570	311	28.2
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.12		456	.12		53	-12		502-	-17		0/5-	-12		1658	-12		232	-12	;	-81	-15		281	- 75		285	12		4.	-12		-517	-12	:	-517	:	-198	-12		-517	-12		-454	-12	:	349	-12		
27		203	27		0.	27		666.	7.7	;	165.	27		-531	27	į	-531	27	:	-182	27		318	27	:	188	27	:	-478	27		-478	27		1865	ì	-478	27		-478	27		-109	27		-415	27		
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-73		551	.73		116	-73	į	- 659	-73		-630	-73		361	-73	;	-630	.73		-630	-73		2224	.73		-630	-73		-577	-73		36	-73	į	.577		415	-73		-577	-73		-200	-73		2338	.73		
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-164		-548	-164		. 793	-164		2036	-164		410	-164		÷	-164		902	-164		- 722	-164		. 722	-164		-722	-164		284	-164		-699	-164	;	699.	F0.7	2117	-164		-669	-164		909-	-164		-182	-164		
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438	•	54	438	•	-190	438	•	418	438		-120	438	•	610	438	•	-120	438	•	-120	438	•	436	438	•	-120	438	•	-67	438	•	1919	438	•	744	•	339	438	•	726	438	•	4	438	•	4	438	•	
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	165	41	ì	597.	4	765		;	- 765	41		-765	4		.765	41	100	6.1	:	96-	4		- 765	41		- 165	41		- 765	41	- 765	41		-165	4	- 765	4		-765	41		-69	41	
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	1605	-611		327	-677		323	-617		1605	-677		-1605 -	-611		•			1605	-677		1605	-677		-1605	-677			-677			-677		Ť	-677		•	-677		-250 -			-1605 -			•	-677		-1605
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626	-732	-962	-352	-732	069-	-352	207	-352	-732	261	-352	-732	66-	-352	. 732	196.	-732	- 929	- 352	.732	134	- 352	732	.53	352	-732	938	-352	-732	7267	- 732	-890	-352	-732	-870	- 352	-732	077	.352	-732	-897	-352	.732	.1229	252.	135
1.20	-6794	-788	-178	-8794	-116	-178	-788	-178	-8794	-788	-178	-8794	-788	-178	-8794	907	-4216	506	-178	8718	541	178	6718	755	178	.8718	- 755	-178	-3958	921.	-8627	530	-178	-4783	969-	B/1-	.8579	060	-178	-4313	-723	-178	.8645	-1055	178	.6372
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-153	-25	585	-153	. 55	585	551.	0 2 2	. 153	.25	585	-153	15	585	-195	272	585	-153	-25	585	-153	-25	585	-153	116	585	153	. 55	\$85	.153	- 25	585	101	585	-153	1001	585	-153	884	585	-153	-25	585	-153	.25	585	-153	.25
-3313	-238	372	-3313	495	372	- 1313	,	- 1313	171	372	.3313	134	372	-2981	-124	372	-3313	-238	372	-3313	187	372	3313	171	372	3313	534	372	3313	-238	372	27.5	372	-3313	-238	372	-3313	179	372	-3313	-238	372	-3313	56.	372	.3313	94
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-8794	13	-178	-8794	-100	-178	46.6	007	-8794	-788	-178	-3974	-76	-178	-8702	-652	-178	-8794	- 188	-178	-8794	- 788	176	8194	188	178	8194	168	.178	8794	- 788	-178	200	-178	-8794	-788	.178	-8794	- 788	-178	-8794	-788	-178	-8794	- 788	-178	-8794	-788
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-677		72	-677		86	-611		-165	-617		-601	-677		-705	-678		335	-619		-1756	-617		480	-617		221	-617		233	-611		-1067	-617		-1657	-617		-1805	-617		-3106	-677	
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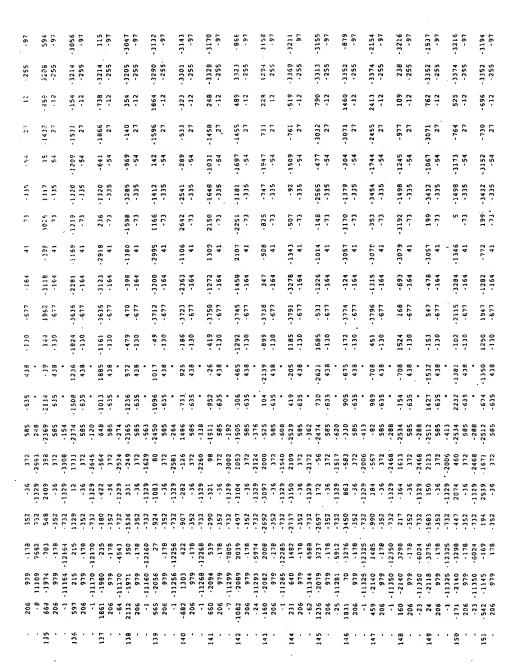
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3374	.255	. 3352	-255		-3352	-255	:	35.50	5627	311	-255		-3306	-255	3000	256	1	-3296	-255		961	255		.455	.255		.1262	.255		-1237	-255	.1103	-255		-3106	-255		-3138	-255		7905-	557-	- 1141	-255		965
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18	ž.	1194	54		1800	-54	0,01	1435	5	2616	.54		1909	. 54	243	45.	;	-101	-54		19	.54		182	.54		-1379	-54		-264	- 54	1416	-54		262	-54		-292	40	F		,	521	-54		609-
-634	335	-363	-335		255	-335	0171	2116		-472	-335		4 8	-335	=		;	.584	-335		239	-335		-540	-335		-237	-335		1977	-335	2266	-335		-368	-335		2434	. 335	900	9007	n	.361	-335		.3190
715	7.	1318	-73		-159	-73	9		:	346	٠٠.		1043	.73	2358	.73	•	3002	-73		1494	٤٢.		733	-73		-3079	-73		-3027	.73	1615	.73		1211	-73		1609	?	0000	. נני	•	2959	-73	:-	- 686-
2338		488	4.1		-663	41	.00	41	:	-775	41		176-	‡	005	4	!	-1239	41		.1239	41		-425	41		. 3968	4,		. 2914	41		41		- 996•			- 232			2 6		2846 -			-232
-1315	70	.379	164		-1017	-164	124B	154	5	-987	-164		-1212	-164	23.94	-164		-3206	-164		3206	-164		784	-164		. 1716	-164		172	- 164	-430			-183	-164		942	+01-	1000	1,64		1502 -	-164		2446
359	è	498	-677		- 3774	-677	, 556	.677		219	-677		-3728	-677	-247	-677		1511	-677		- 2064	-677		٠.	-677		.3683	-677		3631	//9-	-79	-677		1958	-677		3560		1926	-673		1001	-677		1189
.463) · ·	-864	-130		-302	.130	105	130	:	36	.130		-684	-130	-660	-130		878	-130		285	.130		1815	.130		437	-130		-167	061.	-630 .	-130		1507			. 1911	061	. 191	130	2	.516	-130		.715
-619	, ,	-719	438	•	- 372	438	107.	438	•	-920	438	•	-1048	438	-291	438	•	-139	438	•	.184	438	•	1373	438	•	1764	438	•	-477	D *	-359	438	•	1724	438	• !	147	9	. 187.	438	•	1075	438		-578
1672	n •	1865	-635	•	200	-635	9.50	-615	•	-1298	-635	•	-3687	-635	-3705	-635	•	-2234	-635	•	-1056	-635	•	-2753	-635	•	-3642	-635	•	.3589	c;e.	.3573	-635	•	3486	-635	•	3519		.357	.635	•	1120 -	-635	•	3491
.363	C 8 8 C .	-2512	585	-263	-1543	585	764		-242	32	585	.242	.259	585	-221	585	-226	278	585	-311	2456	585	-198	83	585	-168	625	585	-168	2369	.291	2353	585	-194	1368 -	585		•		2222	585	-306	878 -	585	.371	543
-2296	3.2 2.15R	-2725	372	.2587	-1497	312	1260	372	2696	.2703	372	-2696	-2679	372	1036	372	2786	1426	372	2368	2228	372	2961	2635	372	3182	-725	372	3182	- 646	2453	504			•	372				•			-150	372	2142	99
1757	1329	.329		1329					-1329																									•			•	•		٠.		•			•	
258	732	1430	-352	-732	1601	255.				_		-732		.352		.352			. 352														-352			352						732				•
3298	5024	2521	.178	12325	. 255	8/1.	3253	-178	12299	- 2505	.178	5939	R32	-178	.351	.178	. 5607	3220	178	5889		_		2444							4849			4134	3030	178	05.00	2/3	02170	-833	178	7703	. 5908	.178	1708	
.2140	11350	-1145	979	11325	6117-	717	. 2096		11299		616	11299		979		616				•	197								•			•	979		٠							•	•		•	1876
.1595	•			7					•			•		907	305		•			•						•			•		٠			•		506						7			7	
221		222	•		577		224		•	225	•		526		227			228 -			529			230			731					233			234					236			237 -1		. ;	873

3215	76.	3121	- 97		-3216	-97	3166-	16.	,	-3216	-97	,	.97		-3216	-97	.3216	-97		.3216	.97	3100	4175-	. 67	-3216	-97		-3216	16.	-3216	-97		-3216	-97	-2140	-97		-2140	-97		-1537	-97	
238	255	97.0	. 255		-3374	-255	916	255-		238	-255	;	-255		1178	-255	2406	-255		238	. 255		1023	-255	4022	-255		4550	-255	1990	-255		-3374	- 255	-3352	-255		-3352	-255		-3352	-255	
1961	. 12	0,00	.12		-3131	.12	777	;	;	-917	-12	į	- 313		-145	-12	149	.12		1498	.12		1167	-12	472	.12		- 509	-12	1306	-12		2191	-12	594	-12		-1604	.12		-184	•12	
2179	5	6	2.50.2		2552	27	į	, ,		699-	72	;	-1044		755	27	.612	27		7	27		7771		1983	7.2		-350	2.1	282	27		- 764	27	-2438	27		535	27		-538	27	
4) 6)	54	Ç	5.5		-327	- 54	1040	95.	;	-894	-54	ě	-54		485	-54	119	- 54		-528	-54		bb/1-	4	-1314	-54		-1040	. 54	-1744	-54		-570	-54	-535	-54		104	-54		783	-54	
1002	. 335	2346	-335		-742	-335	1400	526-		-697	-335	;	.335		-2610	-335	-1498	.335		-1002	-335	;	5	-335	-1498	-335		-1498	-335	-697	-335		.1616	-335	ur i	-335		-196	-335		282	-335	
6.	7.3		.73		-1500	-73	2100	.73	•	-1164	-73	,	-318/		519	-73	-1164	.73		-1164	.73	:	-1164	-73	-1164	.73		422	-73	.353	-73		-891	-73	115	.73		-862	-73		377	-73	
526	7		, ,		2131	41	0360	76.20	•	2878	4	í	41		-583	41	1346	4		-3079	4	ì	1346	41	-1346	41		285	43	-581	7		-169	4	374	4		-1426	41		1667	41	
1335	-164		-164		-1315	-164	4 9 0	164		- 901	-164		-3278		-1434	-164	.1900	.164		-622	-164		- 3284	-164	-2432	-164		-1315	-164	-3284	-164		-3284	-164	-1116	-164		-117	-164		-101-	-164	
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.1361	438	• 6	438	•	-1381	438		96.5	•	-1381	438	•	438	٠	-2681	438	1161	438	•	-1161	438	• ;	1381-	438	-438	438	•	-251	438	- 708	438	٠	-2681	438	1360	438	٠	1915	438	•	-536	438	•
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22.5	5 3 2	-288	585	.288	-1558	585	-298	המי	-288	424	585	-288	585	- 362	.1558	585	.2534	585	-288	1213	585	-288	652	585	355	585	-288	.250	585	5.94	585	-288	1075	585	.53	585	-263	-2515	585	-263	-2515	585	.413
2747	112	2468	372	2458	1527	372	-2468	נננ	.2458	.822	372	-2468	372	-2172	-2747	372	-2296	372	.2468	197	372	-2468	9/8	372	-1527	372	-2468	.2747	372	.2747	372	-2468	-1527	372	-2468	372	-2587	-1497	372	-2587	-2725	372	-2006
1359	. 36	1329		-1329	.1169	- 36	1329	5616.	-1329	.1169	.36	.1329	- 2286	-1329	-3155	.36	1169	.36	-1329	.3155	-36	-1329	3155	-36	103	-36	.1329	-2293	-36	.364	- 36	-1329	280	- 36	937	-36	-1329	1154	-36	-1329	-1136	- 36	-1329
.1952	352	.732	.352	-732	.533	352	732	144	- 732	.77	-352	-732	.352	. 732	1452	-352	1220	.352	.732	100	-382	-732	- 44.	-352	.67	-352	-732	-295	-352	- 1930	-352	-732	.3471	-352	. 1450	-352	.732	1306	.382	.732	1743	- 352	-732
-12304	.178	12350	.178	12350	.3298	-178	12350	V 40.	12350	1225	-178	7857	.1221			-178	95.	.178	-12350	.3298	-178	12350	507	12350	7	.178	-12350	.1485	-178	-1485	-178	-12350	.707	.178	.1568	-178	.12325	-1369	-178	.12325	.214	-178	-12325
.11304	979	.11350	979	-11350	1391	979	11350	97/	-11350	1720	919	11350	979	-11344	1625	979	2344	979	.11350	3312	979	.11350	867	979	-2140	919	-11350	36	979	867	979	-11350	1787	979	-11350	979	-11325	-2118	919	-11325	-2118	919	.11325
1.	506	1.	206	7	-1467	206	- 5	1981.	-1	-2456	506	Ċ.	206	7	-561	206	1001	205	•	- 789	506	7	.1680	206	-1680	206	-	-2913	206	.2913	206	7	-566	506	-23	206	-7	.510	. 206	•	-441	206	7
, 20.	,			•	506		٠ ;	2		208	•	' ;	503	•	210	•	. :	:	٠	212	٠	. ;	213		214	•	•	215	•	216		•	217	•	. 81	•	•	219	٠	•	220	•	•

16.	727	. 97		-653	- 97	.;			564	.97		168	-97		1135	•	1135	-97		1710	۲.۵		1028	97		2987	6.	3336	-97	;	1964	.97	2818	.97		3197	-97		669	-97		-3174	-97		069-	76.
-255	1516	- 255		-3395	-255	,,,,	2666.	3	338	-255		586	-255		355		1212	-255		65	255		1520	255		3364	557.	3000	.255		3940	-255	-3352	-255		274	-255		-3374	-252		2039	-255		B	557
12	1057	-12		-1666	-12		, , , , , ,	•	-3069	-12		-3084	.12		6677	;	-1588	-12		1463	Ë		162	12		3121	7	. 7637	-12	;	-357	-12	-1171	-12		-163	-12		-,196	.12		-894	-12			-17
2.7	76	2.7		175	23		0/67-	•	-668	27		219	27	6	2 6	•	935	7.7		719	5.2		1047	2.1		36	12	1441	27		1868	27	2289	27		410	27		1062	27		1217	27		2 5	7.7
-54	214	.54		273	.54	;	61/1-	5	-232	- 54		443	-54		1001	ŕ	1911	-54		. 104	-54		-420	-54		428	- 54	0 7 1	1 2 4	;	-463	.54	-506	-54		-154	- 54		-1164	-54		1382	-54		6/17	.54
-335	1987	-335		27	-335		5067-		-1405	-335		231	-335		7001-		- 10	-335		830	-335		716	-335		-692	- 135	730	. 335)	-1694	-335	-14	-335		-322	-335		-3454	-335		-3413	-335	;	- 1413	-335
-73	.79	-73		-3213	-73	0	6977	-	-809	.73		-2257	-73	;	2416.	?	-3118	-73		-714	-73		-426	-73		-3182	7.	1167	.73	!	-3192	-73	.1131	-73		-635	-73		-1759	-73		-3151	٤٢-	;	1411.	٢/٠
7	909	7		.117	7	:	747-	÷	2149	41		2714.	5		758	;	-232	41		290	4.1		423	. 41		-1083	4	5	1 4		-1346	1	-1313	4.		1458	41		2283	4		599	4	į	946	41
.164	130	-164		-211	-164	:	571		-415	-164		-2384	-164		7 7 7	7	.1801	-164		-3047	-164		-840	-164		-3273	-164	0 20 0	-164	•	-3284	-164	-1282	-164		-3262	-164		-955	-164		-1291	-164		- 3242	-164
.677	. 771	-677		.1370	-617		. 44		.3733	-677		-3748	-677	}	96/5-	6	-3721	-677		-3559	-677		-3524	-677		-3786	-677	1221	-677	•	-3796	-677	-2103	-677		-282	-677		-1360	-617		-3754	-611	į	154	-677
-130	~	.130		1646	.130		2448	2	1896	-130		254	.130		7571-	7.70	664	-130		1719	-130		-522	-130		-1333	.130	900	-130		-545	-130	968-	-130		5.	-130		-688	-130		-949	-130		7.	-130
438	.567	438	•	-2209	438	• ;			-480	438	•	-2144	438	• ;	2/-	,	986.	438	•	-2445	438	•	-1192	438	•	-1280	438	• 2220	438	•	-1161	438	-878	438	•	-1350	438	•	-1381	138	•	-1353	438	• ;	0.50	438
635	. 870	-635	٠	-3776	-635	. ;		•	-3692	.635	٠	-3707	-635	•	37.55	•	.1644	-635	•	.3518	-635	•	.1527	-635	•	-1681	-635	• 666	.635	•	-2288	-635	- 784	-635	٠	.3733	-635	•	-3755	-635	•	-1663	-635	• ;	155	-635
595	195.	585	-455	-2555	585	-318	2167-	. 185	-2472	585	-792	.2487	585	-872	. 363	. 455	-2460	585	-913	-228	282	-1293	-202	585	-1332	-236	585	-429	585	-476	-363	585	-1543	585	-263	-968	585	-413	153	585	-288	- 2493	585	-177	040	28 20
372	523	372	.1885	1345	372	.2339	1154	.1593	-841	372	.1243	.774	372	-1141	1316	. 1885	-2673	372	-1093	-733	372	-757	- 709	372	-731	334	372	- 1959	372	.1831	.149	372	- 583	372	-2587	-405	372	, 2006	1633	372	-2468	2205	372	CI :	781	372
-36	. 1329	. 36	-1329	.1201	-36	-1329	785.	-1329	-661	-36	.1329	-851	.36	-1329	-1757	1129	-1126	-36	-1329	-52	-36	-1329	-1008	- 36	-1329	- 76	36	1329	1001	-1329	-146	.36	-1136	-36	-1329	-590	-36	-1329	-3155	.36	-1329	-3114	• 36	-1329	10 v	- 36
. 352	. 2261	.352	-732	.1177	-352	732	0696	.732	7571-	-352	-732	-110	.352	-732	1851	266.	-1403	-352	-732	-729	-352	.732	-2419	-352	.732	-1451	.352	- 732	-352	.732	. 602	-352	.912	-352	-732	.863	-352	-732	-65	.352	-732	.1690	-352	732	+76.	352
-178	5982	-178	.12350	456	178	. 5073	67.	0.10	.610	-178	-4208	-550	.178	5970	38	2775-	179	.178	. 2475	-590	-178	2040	2257	.178	-6446	2050	.178	-5768	.178	-12322	-1485	-178	- 1452	.178	-12325	-3276	.178	-12325	.2042	178	4915	-1263	.178	12304	9575.	9/1.
616	11325	979	-11350	.182	616	-11374	67.0	52111.	-1117	979	-11278	84	616	11297	1523	-11350	254	616	-11258	.1903	919	-11087	. 824	979	11046	635	626	-11339	979	11322	36	979	902	979	-11325	-2118	979	-11325	36	979	-11350	59	979	-11304	n c	<u>بر</u> بر
206	-2456	206	-1	-1162	506	4	706	907	-2851	206	-63	-871	205	-24	0901.	110	-510	206	-287	-2677	206	-403	. 2641	206	-17	-1816	206	72-	206	-	-1467	206	-1500	206	-	-2892	206	∵	-1282	902.	-49	-2872	206		7/87-	505
•	. 68	: '	•	168	•		6	•	190	٠	•	191	٠	:	192		193	٠	•	194	•	•	195	ı	•	196			<u>;</u> '	٠	198	•	. 66	•	٠	200	•	•	201	•	•	202	٠	٠ ;	707	

9012		607		-843	- 97		-173	6	- 789	. 6.		62	- 97		-3216	, ,	2100			.3216	- 97		-3167	- 97		-592	-97	į	6/8		-907	- 97		-3167	16.	-3194	-97		1399	-97		-100	-97	;	7
349		3306	-255	-3330	-255		-3347	- 255	9911-	.255	}	-3374	-255		-3374	-722	. 2247	300	70.3	-3374	-255		. 3325	-255		-3347	-255	;	-3342		-3364	-255		-3325		-3352	-255		-3325	-255		1143	-255	,,,	ž,
1117		777	-12	.683	-12		-401	-15	-461		1	-716	-12		-1636	77-	1636	;	77.	2544	-12		-22	.12		29	-12		0017-	37.	-1187	-12		-1568	71.	-1111	-12		-738	-12		-2560	-12	:	K111-
-265		556	27	-549	27		-1226	2.3	1502	22	i	1944	27		. 764	7	000	, ,	,	329	27		.152	27		111	27		900	,	.1066	رم برم		1931	¥	-407	27		-730	27		-1532	27	,	200
915		1078	.54	1894	-54		-203	- 54	457		;	- 162	.54		-363	- 54 -	46	2	5	834	-54		1507	-54		-209	-54		1004	5	-2608	-54		946		-217	-54		-695	-54		.350	-54	;	7.7
335		-3386	- 335	-1037	-335		341	- 335	8.0	- 115	1	-480	-335		-185	.355	2690	,	1	293	.335		-1360	-335		-2588	-335	ľ	527.		-65	-335		-373	000	-1465	-335		-1200	-335		-1257	-335	5	P C
679		.70		-1732	-73		349	-73	1752	15	?	-1164	.73		-491	٠,٠	376		?	777	-73		571	-73		-1739	-73		446	?	-348	-73		-1726	?	-1131	-73		-2289	.73		-3213	۲٠.	,,,	0/15-
.1002		269	-	-3034	41		-2341	4	a y	1.4	:	-1887	41		485	4.	1113	1	;	-581	41		816	47		1676	₹	ŝ	06-	;	665	41		- 974	;	913	41		163	41		1965	41	2000	0007
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1376		1086	-130	-1014	-130		-1040	-130	-1512	200	1	-484	-130		-688	051-	111	1 2 2	130	-358	-130		-601	-130		-2058	-130		9501-	27	785	-130		280	2	-753	-130		-212	-130		552	-130	,	0
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.635	•	-1711	.635	1750	-635	•	2069	-635	.1407	.635	,	-159	-635	•	-3755	٠6.35 د ر	1560	200	C *	-1687	.635	•	-1616	-635	•	-1455	-635	• :	524	•	-2274	.635	•	-3705	7	-1653	.635	•	-46	-635	٠	-921	-635		0001,
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	338	255		.3251	.255		-3347	-255		-3213	-255		293	-255		.3306	-255		-3250	-255		.3088	- 255		308	-255		-3352	-255		- 3325	-255		111	-255	.1152	-255		-3330	-255		-1291	-255		-3306	-255		-3306	-255	
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	e: :	335		1274	-335		-1462	-335		-3293	-335		-571	-335		. 739	-335		.983	-335		-3168	.335		.2573	.335		-1473	-335		-1167	-335		-1670	-335	9211-	.335		-1431	.335		-1107	-335		-3386	-335	į	.922	-335	
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	u.	Ţ		108	7		64	41		475	41		-1174	41		1019	41		- 555	41		1871	4		2372	4		-438	4		239	41		-1033	+		4.1		119	4		-1208	43		-1245	41	;	-3011	4	
	3221	- 154		-674	.164		38	-164		850	-164		378	-164		- 590	-164		1729	-164		1903	-164		404	-164		-1282	-164		-983	-164		9	-164	1500	-164		-1589	-164		-349	-164		-738	-164	:	96-	-164	
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•	113	. 635	•	588	-635	•	-624	-635	•	-1535	-635	•	-1630	-635	•	-1627	-635	•	-3630	-635	•	93	-635	•	.370	-635	•	92	-635	•	-3705	-635	•	208	-635	97.	-635	•	397	-635	•	427	-635	•	-882	-635	• ;	-201	-635	
 -	17	585	474	-178	585	.641	-2507	585	- 244	.2373	585	-1059	1194	585	-678	601	585	-714	-415	285	926-	616	585	-1282	.2487	585	-437	.2512	585	.263	-2485	585	-307	-2490	585	0.5	585	-263	-2490	585	-242	1449	585	-323	-535	585	-224	454	585	677.
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1611			2934	t,	650	76.		-843	- 97		-843	.97		.843	'n	3148	-97		3098	.97		868	D1		S	۲ó		428	-97		1099	- 97	-564	-97		174	-97		2768	- 97		2/26	- 97	;	7 1	-97	;	1368
1011	900		3325	-355	3306	-255		311	-255		310	-255		321	667.	1143 -	-255		•	-255		3305	.255		3901	. 255		3955	-255		3212	-255	1048	-255		9262	-255		3209	-252	,	3176	-255	, 00.	3204	-255	;	3162
٠ درد.	2	!	703	. 13	184	-12		149	.12		309	-12		591	71.	51	.12		1674	.12		2068	-12		195	-12		-2428	-12		-332	-12	. 1292			- 2002	-12		- 5962	-12			-12		961-	-12		147
טראני.	22.		.3043	2.7	-1477	27		-695	27		-3048	27		-3048	,	-658	27		-2364	27		-1402	72		-1336	27		-1317	27		597	72	2164	27		94	27		-1565	2.2		-1869	1.2		160-	2.1		1231
.1100			288	.54	-915	- 54		.1186	-54		-1680	-54		-3129	F. 7	-1934	-54		-1574	-54		-1646	5.		-1582	.54		.981	-54	į	151	- 54	0.5	-54		260	-54		-1523	- 54		9 1	•5.	,,,,	1771	.54	:	- 52
4.0	33.5		-433	.335	.3386	-335		.3410	.335		-3410	-335		-1431	crr.	-1395	-335		-1319	.335		.3386	-335		-1327	-335		.1058	.335		-2484	-335	-2295	-335		-2131	-335		-469	-335		2771-	-335	,	- 3204	-335		-3242
0111			.3143	.73	-3124	.73		-3148	۲,		-832	.73		-1732	?	85	.73		-199	-73		-3124	٤٢٠		297	.73		571	-73	;	-939	- 73	-1056	.73		-772	-73		-3027	-73		667-	- 73		1/17-	.73		429
3005.	;	:	.324	7	926	7		514	41		-3034	41.		-1280	*	-3011	41		-2960	41		-1468	4.1		-2961	4.1		- 385	41		573	4	r,	4		- 504	41		-413	4	:	9111.	41		5777-	41		-2867
9021.	- 164		. 3234	-164	-1212	.164		-3239	.164		651	-164		1025	*01.	- 955	-164		86	-164		-18	-164		84	- 164		2156	-164	;	2397	-164	405	-164		438	-164		-1215	. 164	ě	· :	- 164	,	7	- 164	,	- 390
7 7	. 677		554	.677	30	-617		603	-611		-2090	.617		680	Ç.	62	-677		-1306	-677		-3728	-677		-810	-677		-234	-611		.3634	-611	-1807	-677		-1619	-617		-3631	-611		1665-		3636	0700-	1.19-	,	- 3584
. 979			-535	-130	-445	-130		9	-130		1199	-130		1274	- 130	1038	-130		1394	-130		-3182	-130		.1839	-130		-1620	-130		-312	-130	-1754	-130		.283	-130		. 993	-130	Ş	196.	-130	40	266	-130		-1062
90	478	•	-179	438	-2613	438	•	.1105	438	•	.1318	438	•	-1316		-174	438	•	284	438	•	204	438	•	- 75	438	•	765	438	• ;	510	438	1126	438	•	2211	438	•	2217	438		5967-	9,58	, ,,	657.	438		-1996
	5.5			•	•	-635		-423			-316			-1009			-635			-635												-635		-635		•	-635		-3589			040			1011	-635	;	-317
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21.	202	-25	200	206	2177	206	-	1402	206	7	.1411	206			202	.404	206	-50	.725	206		-307	206	- 76	-727	206	-46	.198	206	- 30	-825	205			-455	-2465	206	-19	285	907	7 5	200	402	יי ל	7 4	007		ĵ
11.7	:	•	118		119		•	120	•	•	121	•	•	122		123	•	•	124	•	•	125		•	125		'	127	•	. ;	128		129	•	•	130	•	•	131	•	:	132	•	. :		•		7

	30,35		-2997	.97		וולי	-97		91	-97		-491	- 97		569	-97		1008	-97		-685	. 97		893	16		3211	0.		. 3211	-97		-3211	- 97	466	-97		-3211	-97		-162	.97		946	-97	6	-972	, ,	
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	575		.2913	-12		-1442	-12		-1253	-12		.2981	-15		-1464	-12		-1157	-12		. 31	12		897	<u>:</u>		143	7		207	-12		-526	-12	1744	-12		1805	-12		389	112		517	-12		-2503	- 12	
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į	595.	5	1332	-54		2138	-54		218	-54		551	-54		354	-54		150	-54		642	.54		1570	7.0		2062	ŝ		-349	-54		-1509	- 54	121.	- 54		-1427	-54		-1710	-54		-860	-54	6	. 828	, V	
	527		-2430	.335		-640	-335		-3317	-335		-1687	-335		-3236	.335		-2256	-335		-678	-335		.3418	.335		. 3449	-335		-3449	- 335		-1495	-338	1405	-335		-1495	-335		-778	-335		-1585	-335	;	-143	- 335	
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	2698	;	156	41		-378	41		-274	41		-355	41	•	- 904	.		-2779	41		-1935	4		.652	41		-3074	4.		-3074	₹		-3074	7	2004	1		-578	41		-46	41		-1310	41		-3029	5	
	-1206		.71	-164		-218	.164		01	-164		309	.164		469	.164		-554	-164		-1438	-164		-1294	-164		451	-164		-1312	.164		-2425	-164	5111.	-164		-150	-164		-371	-164		185	.164		-3234	-164	
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2539	1854	2414	2066	372	-1531	170	372	-2256	-174	372	-2088	914	372	-2112	2061	372	-1341	225	372	-1004	2260	372	- 804	2124	372	-1551	28	372	.2572	.456	372	.2572	919	372	2762-	372	-2572	.839	372	-2572	900	372	.2683	1010	372	-2683	385	372	4617-
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. 732	1479	732	.3253	-352	-732	-562	.352	.732	574	. 352	-732	828	-352	-732	57.1	.352	-732	197	-352	-732	- 368	-352	.732	515	-352	-732	1578	-352	-732	2254	-352	-732	367	-352	261.	-352	-732	-1712	.352	- 732	-128	-352	-732	617	.352	.732	406	-352	- 134
-4123	350	- 3941	353	-178	-3928	-1041	-178	-5410	1821	-178	-4207	2524	-178	-3433	-659	.178	-2520	-2999	. 178	.1897	-1243	178	.11936	588	-178	-12310	- 704	. 178	-12344	. 167	-178	.12344	-1482	-178	1594	-178	-12344	1721	-178	.6021	2148	-178	-12320	-1265	.178	.5980	-3248	178	777
-11203	-1950	-11144	.1921	979	-11099	272	919	-11167	267	919	-11196	-1989	919	-11183	-1922	919	.11108	.800	919	-11016	.1772	919	-10936	2104	979	-11310	. 2135	919	-11344	-2135	979	-11344	2135	979	71344	616	-11344	-2135	919	-11344	-2113	979	-11320	-2113	919	-11320	2091	979	11294
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-130		.5	-130		.821	-130	.624	-130	?	1163	-130		1592	-130	-267	-130		-595	.130		-236	.130		-619	-130		1234	061.	1354	-130		.1173	-130	18	-130		1067	-130	. ;	- 916	-130		- 916-	-130	•	. 021-	
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1101	27		-459	7.2	6	826.	7.7	901	207	7		.05-	23		-1464	2.1	.00	27		.7.	72		-535	27		169	27		- 184	27		-1020	27	ראם	27		-2548	27		-2134	27		• 900	7.7	1	-814	27	:	567
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454	577		3624	125		91.5	-611		1107-		į	-174	-611		1011	-677	0.00	-677	,	-2044	-677		-3646	-611		-392	-677		-3652	-617		-3560	-677	9	-677		1142	-611		-1769	-611		1046	-611		-2094	-677	ţ	179
-2341	-130		-3078	-130	- 3	-646	-130		-2388	- 130	į	926	.130		-1749	-130	0.3		•	-212	.130		- 75	-130		372	-130		-673	-130		-470	-130	1	130		-545	-130		-2956	-130		.399	-130		1213	-130		1355
-1225	438	•	4	438	•	-854	438		15.	4 58	•	-1311	438	•	699-	438	. 1011	418	•	-2558	438	•	453	438	•	666-	438	•	-264	438	•	.570	438		4 . A	•	818	438	•	1916	438	•	-1234	438	•	.738	438	•	1105
.1520	-635	•	-516	-635	• ;	-1577	- 635		6617.	613	•	104	-635	•	-155	-635		5,6	•	-204	-635	•	-2736	-635	•	-3604	-635	•	-3611	-635	•	-1473	-635	. ;	5635	•	-1265	-635	•	-2513	-635	•	.1114	-635	•	815	-635	• ;	341
1069	585	116	2779	585	-633	3521	585	115.	649	585	334	1041	282	-467	-324	585	14.	4 6 6	-226	-2411	585	-286	-2384	585	.370	-2384	585	-479	-1457	585	-372	847	585	112.	585	-255	-1990	585	.547	611	585	-897	-2383	585	-1087	- 355	585	-231	240
1640	372	-3122	2220	372	-1493	- 142	372	8957-	699.	372	-2274	-1314	372	-1854	-837	372	- 1898	173	-2786	1164	372	-2476	25	372	-2145	334	372	-1824	83	372	-2139	. 735	372	5/87-	3,25	-2628	320	372	-1664	133	372	-1111	-250	372	.918	-104	372	-2755	A C P
- 1017	.35	.1329	192	-36	1329	644	- 36	-1329	2102	9	-1329	2574	.36	-1329	-1130	.36	-1329	11.	-1329	2312	.36	-1329	2432	-36	-1329	- 792	-36	-1329	-2188	. 36	-1329	-676	.36	4761-	9697-	-1329	-427	.36	-1329	-2861	-36	-1329	-218	. 36	.1329	-47	-36	-1329	9 9
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. 4.7	9 6	11215	-1968	616	11152	- 2062	976	19711	445	616	11288	.1117	616	11288	.2108	919	+1611	2 0	11294	-1074	616	11208	1990	979	111177	-1990	979	11177	1997	979	11185	-1904	979	11085	650	10835	-1596	616	10733	-1846	919	11022	-1989	979	11182	-1141	979	11333	-2040
2305	206	.52	-1450	506	- 28	.38	206		1258	506	- 24	-952	506	-24	.1435	506		1001	. 72	-2790	206	. 53	-1473	206	. 55	- 803	306	. 77.	-575	506	.172	- 700	206	- 309	962-	-220 -	-1221	206	7	480	506	- 74	1593	206	99	-697	506	- 40	-2056
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	131	5.2	-1138	27		-209	7	-2793	27	,	-337	27		-1263	•	-151	27		434	27	6	5 6		978	27		1998	27	428	27		976	27	į	19,	•	-636	27		- 59	27		363	27
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-2410	+ 1 2 ye	-1451	-588	372	-2237	.835	-1407	666	372	.3349	438	372	-2635	372	.2191	-429	372	-915	77-	372	21.1	372	-1793	.1430	372	-1843	- 344	21.6	-802	372	-1356	-284	372	-1320	372	-1487	.456	372	-2683	-828	372	.2052	-830	2531
.1329	. 518	.1329	104	- 36	-1329	-3024	-1329	-2856	-36	-1329	-79	.36	-1329	116	-1329	.890	-36	-1329	-1073	-36	4,261	98.	-1329	1006	-36	-1329	315	1130	.351	-36	-1329	532	. 36 .	6761-	96-	-1329	-313	-36	-1329	-316	-36	-1329	1003	1329
732	1575	. 732	.660	. 352	-732	.1315	-732	.1496	352	. 732	315	-352	757	352	732	-1100	-352	. 732	1269	352	108	.352	-732	- 608	-352	. 732	11	200.	. 558	352	732	269	-352	-514	.352	-732	-1407	-352	-732	-2214	. 352	-732	155	.732
- 5674	. 205	-4559	.1352	-178	-4401	-1334	-2384	-273	.178	.1983	. 76	.178	9576-	B21.	6893	1491	178	.5758	1754	178	1279	178	6019	2528	.178	2699	-1504	0,1.	519	.178	-5039	1444	-178	.378	178	4508	929	.178	12291	1437	-178	4116	1361	5817
-11141	920	-11149	-2040	979	-11236	65.0	-11202	.811	979	11016	.1478	979	ARCOT .	626	10628	.1734	979	10893	-2040	6/6	5651	616	11329	430	979	11351	510	11351	. 995	616	11206	819	979	5.50	616	11304	87	979	11291	-2093	979	11297	9707.	11215
-29	976	. 69	-1553	506	17.	206	.307	.32	206	-422	-1182	206	201-	206	13	19	206	- 28	821	206	1 20	206	- 23 -	1635	506	- 53	296	.148	.1645	506	. 45	-818	206	-2872	206	- 65 -	-1175	506	7			. 98-		.26
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	-255		17.	255	1331	4 7 7 7	3	-3321	-255		-1301	-255		378	-255		100		239	-255		-3344	-255		334.1	.555		252	557-	-3328	.255		-3333	667-	-14	-255		-3349	-255	;	309	667-	1064	7 0 7 7	cc>.	ç	-255	;
-	13		1545	2	1560		•	605	-12		-236	-12		-1063	-12		70.1	ĭ	-1112	-12		336	.12		1293	.12		- 372	71.	-1091	-12		7 5	71.	-1605	-12		-738	-12	,	- 967	71.	3004	***	71.	.1689	-12	;
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	.154		516	- 164	9966	2007	701	-3231	-164		-1860	.164		.351	-164	į	127	7	-511	.164		-1874	-164		-543	.164		-110	- 164	575	-154		-2399	- 164	-1189	-164		-1283	-164		-3236	164	24.2	186-	104	2,00	-164	;
	-611		.3792	.677	1743			.700	.677		-2077	-677		-2109	.677		2616		-3787	.677		-3766	-677		-3766	-611		-3761		-569	-677		-3755	1/9-	-1000	-677		-1342	-617		-3748	.611	0,00	25/7-		2000	-677	;
	130		.141	.130	6	210,	007,	.978	.130		.246	.130		-846	-130	6	2002	25.	-740	-130		-350	.130		-138	-130		.501	-130	-487	-130		196	061.	1265	-130		1622	.130		. 235	061.	5	919	7.130	1571	.130	;
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	585	292	2531	585	. 255	· ·	.335	1206	585	-212	539	585	.558	1735	585	.423	1636	-423	669	585	-247	946	585	- 362	2180	585	-451	181	585	-2488	585	-419	198	.339	-962	585	-386	-331	585	-244		280	555	967.	282	90-	585	3
	372	.2450	- 2744	372	. 2571	, ,	272-	-1462	372	-2868	-2692	372	.1641	-1948	372	-1977	55/7	7161.	.1523	372	.2666	- 503	372	.2171	- 841	372	1896	.1506	372	-1531	372	-1988	284	312	-2722	372	.2091	-328	372	- 2682	. 62	372	7617	566.	3/2	2017	372	4
	-36	1329	-3152	.35	.1329	777	1329	.1100	.36	.1329	1438	.36	.1329	149	.36	-1329	97 ?	1329	- 362	-36	-1329	.3125	-36	-1329	. 5566	-36	-1329	-441	- 36	-1112	-36	-1329	.308	- 36	-2272	.36	.1329	295	-36	-1329	-3108	96-	-1329	3561.	9	6761	3,6	,
	352	732	731	352	. 732		.732	. 792	.352	.732	- 585	-352	.732	.1365	.352	.732	7.	-352	. 2249	.352	-732	-2715	-352	-732	-2715	-352	.732	-3437	.352	-3425	- 352	.732	-2709	-352	-1149	-352	-732	111ء	.352	- 732	-1650	- 352	- 132	105.	555	30.	352	;
	178	5003	1229	178	-4651	7117	6165	1468	178	12291	2078	-178	12291	290	178	-6026	50 6	-5681	-119	-178	-6023-	.167	-178	-5982	. 97	.178	-5301	2063	.178	2484	-178	.5956	096.	12304	-518	.178	.5984	-518	118	.5984	1419	9/1.	2550	166.	9/1-	מפר .	.178	?
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1291	-255		1179	-255	1781	.255		4727	-255		2092	-255		-3257	-255		. 255		1108	-255		3235	255		1116	255		.3301	-255		-3318	-255		-3344	-255	-3371	-255		-3391	-255		-3371	-255		-3391	-255		.3391
-1271			-2371	- 1.2	.2981	-12		-1255	-12		-1099	-12		143	-12	550		:	-702	.12		٠	. 21		516	12		.3059	.12		-3075	-12		-1601	-12	-1636	-12		-1666	-12		-809	-12		- 950	-12		759
-1381	27		-2925	2.1	1861	27		-1358	27		-846	27		-379	27	907	5	i	-637	27		2953	2.7		278	7.2		-986	27		479	27		-318	7	-555	27		2466	27		1502	27		-312	27		1532
1456			56	-54	-800	150		497	-54		1661	-54		1413	-54	1131	.54	;	-24	-54		149	.54		-377	54	•	217	- 54		-189	-54		-211	ņ	-233	-54		-465	-54		1614 -	-54		2054	-54		187
9781	-335		-27	-335	1351	-335		1354	-335		2490	-335		1201	-335	•	-335		3298	-335		-581	-335		-695	-335		.3381	.335		1282	-335		1293	٠, ر. د	1466	-335		2245	-335		-698	-335		1530	-335		1530
340	-73		533	-73		-73		•	.73		- 595 -	.73		20					•	-73		-237	-73		843	.73		1094			347			805			-73		2194	-73		2953	.73		. 207			3210 -
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3657	611		3628	-677	3645	-677		·	-677		-3690	-617		3679	-677		-677		3639	-677		3657	-617		3738 -			-595			3740	-617		2090			-677			-677		3792			3813 - 1			3813 -1
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-3615	- 635	•	-714	.635	. 723	-635	•	-1543	-635	•	-3649	-635	•	45	-635	.748	-635	•	377	-635	•	1658	-635	•	1833	-635	•	-3682	-635	•	.1657	.635	•	- 834	•	-353	-635	•	906	-635	•	329	-635	•	237	-635	•	1281
1189	585	-114	2302	585	3397	585	.151	2521	582	-276	3156	585	-126	-102	585	761.	585	-108	-2378	585	-202	-245	585	-530	-2476	585	-188	- 325	585	-275	-2478	585	-681	-1531	.451	-1552	585	-423	752	585	-292	18	282	-423	-396	585	-292	306
474	372	-3719	-198	372	-1379	372	.3333	-1807	372	-2524	383	372	-3579	-123	372	. 200	372	-3789	-195	372	-2938	33	372	-1701	.53	372	-3033	23	372	-2525	1756	372	-1411	2055	-1896	- 78	372	-1911	-2765	372	-2450	-2744	372	-1977	-2765	372	-2450	-1556
-3015	-36	-1329	-506	-36	- 584	- 36	-1329	.3010	-36	.1329	-3050	.36	-1329	-801	.36	6261-	.36	-1329	2306	-36	-1329	-3016	.36	-1329	.3097	-36	-1329	-3082	-36	-1329	-3099	-36	-1329	-3125	-1329	-3152	.36	-1329	-3173	-36	-1329	-365	- 36	-1329	-3173	- 36	-1329	-3173
1334	- 352	. 732	2067	.352	51	.352	-732	.3326	-352	-732	486	-352	.732	. 939	-352	1011	-352	-732	.1094	-352	-732	-1332	.352	-732	2663	-352	.732	2654	.352	-732	-2187	-352	.732	542	-732	1501	-352	-732	-2753	.352	-732	.1927	-352	-732	086	-352	- 732	. 980
418	178	. 5544	.247	-178	.855	-178	12182	.1153	-178	- 7695	.1405	-178	.6738	276	.178	23.45	.178	7658	.3141	.178	12176	-1365	-178	7577	-75	.178	- 5029	.794	.176	12270	-1454	-176	.6001	-561	12316	535	.178	12346	621	-178	-6065	75	.1.78	12346	-238	-178	12370	ě
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•	206		.178	.352	-36	372	585	-635	438	-130	-677	-164	4.	-73	-335	-54	27	-12	-255	.97
•	-51	. 9611	.4898	-732	-1329	-2060	-396	-2810	•											
7	-2098	1 -1325	820	.263	-2340	1204	2775	-1076	-139	-2435	-2981	161	1306	-2377	-882	-1297	-865	-992	1731	1027
'	206		.178	. 352	-36	372	585	.635	438	.130	-677	-164	41	٤٢-	-335	-54	27	-12	-255	.97
•	-122	.10407	.3640	.732	.1329	-1376	.702	•	•											
~	-2040		1576	-468	-2753	356	3944	-3352	108	-2847	-3393	-2881	-117	- 926	-3052	-31	-2690	-2729	1991	-44
•	206		-178	.352	- 36	372	585	-635	438	-130	-677	-164	41	٠73	-335	-54	27	-12	-255	.97
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4	.1634		.189	-1239	-2928	-829	3764	-1473	-494	.3022	-3569	211	-43	-2965	-174	-1528	-281	-2904	3856	467
•	206	616	-178	.352	• 36	372	585	-635	438	-130	-677	-164	4	13	-335	-54	27	-12	-255	- 87
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5	-2704		.1282	.1511	996-	1726	1193	.3545	- 505	.3040	-3586		-2869	-2983	-1295	- 192	-1052	-1432	4722	745
•	206		-178	-352	.36	372	\$85	-635	438	-130	-617	-164	\$	٤٢٠	-335	-54	27	.12	-255	.97
	-44	-11116	-5086	.732	-1329	-3310	.153	•	•											
ø	-1866		305	-1497	-1069	2078	553	-3521	-2448	-2026	-3562	-822	133	-2959	-575	95	-635	-1416	2139	2441
'	206	919	-178	.352	-36	372	585	-635	438	.130	-677	-164	41	.73	-335	-54	27	-12	-255	-97
•	-34	-11089	-5433	-732	-1329	-2927	- 203	•	•											
7	-264		665	136	-248	1501	-2307	-1473	-1003	-1782	-3569	-1328	127	-2965	-1284	-1413	-1287	-2904	449	3192
•	206	979	.178	.352	-36	372	585	-635	438	-130	-677	-164	41	-73	-335	-54	21	-12	-255	.97
•	7	-11096	-12096	.732	-1329	-2348	-315	•	•	•										
æ	-838	7	630	-556	-2975	1822	-176	-1500	969	-1813	-584	407	1251	-109	-2433	162	-1000	-2951	-3194	879
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	۰.	-11148	. 7665	.732	-1329	-3799	-108	•	•											
o,	-1279	•	.584	.804	.979	554	3173	-679	2055	-739	-1932	-209	-839	-974	-1308	-107	-2906	-2945	429	-1366
•	206		-178	- 352	-36	372	582	-635	438	-130	-677	-164	41	-73	-335	-54	27	-12	-255	-97
•	.27	-11142	-5808	-732	-1329	.3144	-173	٠	•											
10	15	1116	969	.560	-2969	424	3235	-3568	-2495	-1410	-3610	3903	218	354	-1308	-797	-2906	-1944	1933	242
•	206	979	-178	. 352	-36	372	585	-635	438	-130	-617	-164	43	-73	-335	- 54	27	-12	-255	.97
•	-	-11142	-12142	.732	-1329	-3464	-137	•	•											
11	-1218	735	-822	347	-2975	1567	1089	-3574	-789	-248	-3615		-1159	-1318	-3274	-1329	-2277	-579	1931	-350
•	506	979	-178	-352	-36	372	585	-635	438	-130	-677	-164		5٠	-335	-54	23	-12	-255	-97
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12	-132	226	300	-2559	-2969	1961	1182	-3568	-377	-1809	-3610	684	1930	435	-1308	-2435	-2906	-1621	1225	-347
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•	-178	438	•	287	438	•	-7	438	•	378	438	•	25	438	•	102	438	•	156	•	0
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-84	-30	585	. 78	-24	585	-77	0	585	-74	65	585	-66	199	585	-64	249	585	-61	303	•	•
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	2087	522	257	255		2635	-255		.53			.555	-255		1050	-255	-	-255		•	-255		2441	255		294	- 255	501	-255		2644	-255	2744	-255		-182			•	-255		-503	-255		76
	251	12	248	. 12		282	-12		264	-12		20	-12		1220	-12	2340	-12		1178	-12		1040	.12		997	-12	9110	-12		367			-12		2559			-593	-12		1520			-938
	618	2.	-212	27		-271	27		1067	27		-365	27		828		,	27		•	27		503	2.1		136	1.7	8501	27		1077	27	.641	27		519			-147	27		-126 .			-219
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	463	135	1513	-335		1328	335		149	-335		547	-335		-623	-335	476	33.		.881	-335		.38	-335		959		7	.335		-444	-335	ÿ	-335		-130	-338		-100	-335		774	-338		- 112
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	-409	438	1405	438	•	1330	438	•	724	438	•	118	438	•	513	438	133	438	٠	1462	438	•	536	438	•	909	438	1648	438	•	1058	438	1691	438	•	1423	438	•	862	438	•	-48	438	•	838
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3753	50.	372	1086	372	3038	1771	372	3594	1537	372	2339	1964	372	3442	.44)	372	1446	372	3579	1044	372	3153	-617	372	1765	1286	7/5	2307	372	2251	-597	372	1,87	372	1912	2175 -	372	2413	2196	372	2460	-729	372	2294	.507
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04.	.12		.93	-12	;	389	-12		-222	-12		- 26	-12		329	-12		273	-12		-130	.12		303	12		1050	12		667	-12	,	- 265	-12	36-	-12		-2392	-12		-1158	-12		-211	-12		- 990	.12
17	2.7		-326	27		-2217	23		-111	27		- 972	27		659	27		-880	27		469	27		-1510	7.2		39	27		-1360	2.1		-740	27	699	27		-916	27		-268	27		-1081	27	1	-1073	27
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9636	335		.1489	-335		-874	-335		-804	-335		-831	-335		-608	-335		-210	-335		-356	-335		545	-335		271	- 335		-2692	-335		-333	-335	43.4	-335		185	-335		1238	-335		521	-335	į	194	.335
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. 2467	1545		574	-164		187	-164		747	-164		-2451	-164		311	-164		- 106	-164		-882	-164		-46	-164		.351	-164		-237	-164		-58	-164	683	-164		-1098	-164		-661	-164		207	- 164		-881	-164
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.143	.130		.1494	-130		292	-130		-357	-130		-628	.130		-559	-130		377	-130		413	-130		-1161	-130		368	-130		-395	-130		921	-130	3.68	-130		55	-130		- 65	-130		- 526	-130	į	382	-130
200	438	•	20	438	•	863	438	•	122	438	•	285	438	•	- 78	438	•	602	438	•	763	438	•	1342	438	•	393	438	•	-717	438	•	-23	438	. 692	438	•	1958	438	•	926	438	•	750	438	• ;	23	438
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326	28.5	.244	1515	585	-104	875	282	.97	862	585	-236	94	585	- 99	1401	585	.158	1465	585	- 90	1396	285	-140	-1599	585	.231	335	585	.568	456	285	-255	- 399	585	769	585	-207	159	585	-222	887	585	.293	-687	585	-188	1307	585
2,10	372	.2583	-196	372	-3840	-322	372	- 3945	.1143	372	.2728	701	372	-3914	-526	372	.3267	-626	372	-4051	-1075	372	-3438	- 85	372	-2756	- 780	372	.1620	-1181	372	-2627	518	372	879.	372	-2902	.1086	372	-2810	-1596	372	-2445	.741	372	-3031	-1985	372
35.5	96.	.1329	229	. 36	-1329	- 884	-36	-1329	-2260	-36	-1329	.740	-36	-1329	98	-36	.1329	-2246	.36	-1329	229	.36	.1329	260	.36	-1329	-1452	. 36	-1329	835	.36	-1329	813	.36	551.	-36	.1329	-816	.36	-1329	-845	.36	.1329	1553	-36	1329	1494	.36
Š	352	732	678	.352	.732	353	352	. 732	1210	-352	-732	870	.352	. 732	1064	. 352	732	-77	352	. 732	-1141	.352	.732	554	. 352	. 732	43	. 352	-732	202	-352	. 732	245	.352	707	.352	.732	773	-352	.732	318	.352	-732	066	- 352	.732	477	. 352
6	178	5261	976	.178	-4757	928	.178	-4599	748	.178	11310	.1216	-178	.4083	.386	-178	-4953	289	-178	-5004	681	-178	-5947	729	.178	5259	-306	.178	-4368	136	-178	11473	. 105	178	5206-	178	.5276	-73	.178	11500	-1831	-178	.3850	408	-178	-4840	-690	-178
	979	-10395	-1287	979	-10425	-1294	919	.10370	1244	616	-10310 -	-1307	616	10387	141	979	10299	600	979	10293	404	979	10248	-1205	6 2 6	.10262	-1245	616	10311	69B	979	-10473 -	1423	979	10521	979	.10504	-1401	616	.10501	-1433	616	10539	26	979	10495	1257	616
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.255		6892	.255		.2648	-255		.2689	-255		-2689	-255		-2689	-255		-2648	-255		-2689	-255		-2689	-255		-2689	.255		.2689	-255		-2689	-255		-2689	-255	-2689	-255		-2652	-255		-2628	-255		-1234	-255	
- 12		1159	.12		4	-12		-141	.12		-1321	-12		-476	-12		174	-12		411	-12		. 904	.12		-2446	.12		-201	-12		681	-12		.57	-12	- 346	-12		-1172	-12		- 864	-12		675	.12	
27		266	27		-156	2.7		-372	27		-1307	27		-458	27		-2367	27		-471	27		-1491	27		-609	27		-1454	27		-1433	27		-1464	. 27	-1464	27	,	-287	27		-41	27		133	27	
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-135		.99.	335		2728	-335		-1832	.335		.1852	-335		-2069	.335		-533	-335		-192	-335		-1033	-335		-1209	-335		-1209	-335		-1952	-335		-1262	-335	113	335	;	628	-335		969-	-335		205	-335	
.73		818	-73		-421	.73		421	.73		395	.73		-128	-73		684	٤٠-		-252	-73		7	-73		744	.73		-1270	.73		1458	-73		905	-73	1288	- 73	!	-846	-73		1126	.73		724	٤٢-	
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577		.311	-611		.3070	-617		1767	-611		1454	.677		235	-677		361	-677		-321	-677		.3111	-677		121	-677		.3111	.677		-2917	-611		-428	-677	יווני	-677	:	-652	-677		-1593	-611		-2996	-611	
.130		966	-130		681	-130		773	-130		211	-130		810	-130		1312	-130		749	-130		35	-130		-163	-130		B 24	-130		167	-130		1356	-130	.146	-130		9	-130		166	-130		-118	-130	
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585	.354	1036	585	-134	1486	585	-258	.163	585	.134	235	585	-134	-1849	582	-134	-1808	585	-260	328	585	-134	-1849	585	-134	1849	585	-134	592	585	.134	.1849	585	-134	-101	585	479	585	- 134	93	585	-247	964	585	-116	454	585	.105
372	2200	Ξ	372	.3499	.697	372	2608	- 49	372	- 3499	.312	372	.3499	-831	372	-3499	-415	372	-2598	62.2	372	-3499	483	372	. 3499	- 542	372	.3499	187	372	-3499	-25	372	-3499	.684	372	274	372	-3499	-1360	372	. 2666	186	372	.3690	699	372	3836
. 36	1325	629	.35	.1329	2429	.36	-1329	-2470	36	-1329	.883	.36	-1329	346	- 36	.1329	-823	.36	-1329	261	- 36	-1329	.314	-36	.1329	1356	-36	.1329	-58	.36	-1329	-803	- 36	-1329	.1045	96.	. 602	98.	-1329	-2434	.36	-1329	639	- 36	.1329	278	-36	-1329
352	732	610	.352	-732	609	.352	. 732	183	-352	-732	-218	-352	-732	969	-352	.732	239	-352	-732	.370	-352	.732	.121	.352	-732	.829	.352	.732	536	.352	. 732	827	.352	.732	-1098	.352	-474	. 352	-732	1055	-352	-732	605	-352	-732	.2672	-352	. 732
-178	11477	784	178	-4917	.525	-178	11516	9.4	-178	11565	23	.178	.11565	906	-178	-4899	.2572	-178	11516	-581	-178	11565	514	.178	11565	337	178	11565	862	-178	11565	663	-178	11565	832	-178	465	-178	-5063	102	-178	-4296	991	-178	.4511	437	-178	-5483
616	.10477	1155	979	10565	338	616	-10516	.1455	919	10565	7.3	919	10565	-1409	616	10565	-37	979	10516 -	-1455	919	10565 -	647	979	10565 -	368	979	10565	179	919	10565 -	-816	979	10565	.752	979	. 50501	979	10565	-1418	979	10521	-806	616	10492	-1340	919	10428
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	1512	.130		739	-130		858	-130		.33	-130		154	-130		105	-130		-831	-130		673	-130		358	-130		498	-130		626	-130	A A	.130		851	-130		- 91	-130		689	-130		287	-130	
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- 134	.11	582	.134	-1800	582	-118	1800	585	-290	346	585	-192	520	585	-134	-1849	585	-134	276	585	-134	124	585	-134	-1849	585	-134	818	585	-134	173	585	451-	585	-134	1280	585	-134	006	582	-134	-24	585	-134	1278	585	.134
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.33	2	.1329	.597	.36	.1329	461	-36	-1329	-1851	-36	-1329	-756	- 36	-1329	9 20	-1129	1186	-36	-1329	476	-36	.1329	305	-36	-1329	265	-36	-1329	-809	-36	-1329	1139	3330	-271	- 36	-1329	.1030	• 36	-1329	-1172	-36	-1329	-604	-36	-1329	1187	.36
er er	352	732	829	.352	-732	536	-352	-732	.163	.352	-732	-224	-352	.732	6,47		- 96	-352	.732	-213	.352	-732	-192	.352	.732	- 552	.352	-732	66B	-352	-732	- 935	.352	-1975	- 352	- 732	-924	-352	-732	-1238	-352	-732	.152	-352	732	52	-352
-	175	4750	1345	.178	-4354	623	-178	.5599	1029	.178	-4638	634	.178	-4442	940	4043	296	-178	-4366	1527	.178	-5578	-438	-178	-4984	739	.178	11447	816	-178	11471	613	178	17511	.178	11565	131	-178	11565	- 660	.178	11565	-862	-178	11565	- 785	-178
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315		135		.303	- 115		-798	-335		-114	-335		-2677	-335		- 641	-335		.763	-335		1200		.335	-335	.335	.335	.335	.335 .335	.335 .168 .335 .2077	.135 .168 .335 .335	.135 .168 .2077 .2077 .335	. 135 . 168 . 135 . 135 . 135	. 158 . 168 . 2077 . 335 . 937	. 135 . 168 135 	.335 .158 .207 .207 .335 .335 .335 .335 .335	.1158 .135 .135 .135 .135 .135 .135 .135 .135	.1158 .1359 .2077 .1359 .1359 .1359 .1359 .1359 .1359	.158 .168 .335 .335 .335 .335 .335 .335	.1158 .168 .1159 .1159 .1159 .1159 .1159 .1159 .1159	.1168 .1168 .2017 .2017 .3156 .3156 .3156 .3156 .3156	. 1168 . 1355 . 1356 . 1356	.168 .135 .2077 .135 .135 .135 .135 .135 .135	. 135 . 135	.158 .115 .2077 .2077 .115 .115 .115 .115 .115 .115 .115 .1
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wdef(cpp32,protein,'CPP32').
wdef(crkl, protein, 'CrkL').
wdef(ctf, substance, 'COOH-terminal fragment').
wdef(cytokine, smallmolecule, cytokine).
wdef(cytosol, structure, cytosol).
wdef(djnk,protein, 'DJNK').
wdef(djun, protein, 'DJun').
wdef (dynamitin, protein, dynamitin).
wdef(erk, protein, 'ERK').
wdef(eto, smallmolecule, 'ETO').
wdef(etoposide, smallmolecule, etoposide).
wdef(fad, disease, 'familial Alzheimer'''s disease').
wdef(fyn, protein, 'Fyn').
wdef(gdp, smallmolecule, 'GDP').
wdef (gelsolin, protein, gelsolin).
wdef(qp120,protein,'qp120').
wdef(grb2, protein, 'Grb2').
wdef(gst, protein, 'glutathione S-transferase').
wdef(gtp, smallmolecule, 'GTP').
wdef(hsp70,protein,'HSP70').
wdef(human, species, human).
wdef(ikk, protein, 'IKK').
wdef(inactivated, state, inactive).
wdef(inactive, state, inactive).
wdef(jnk, protein, 'JNK').
wdef(jnk, protein, 'JNK').
wdef(jnk2, protein, 'JNK2').
wdef(kap3, protein, kap3).
wdef(kdakt, protein, 'KDAkt').
wdef(kinase, protein, kinase).
wdef (kinectin, protein, kinectin).
wdef(klc,protein,klc).
wdef(lamin, protein, lamin).
wdef (myosins, protein, myosins).
wdef(nmdar,protein, 'NMDAR').
wdef(nmdar2b, protein, 'NMDAR2B').
wdef(ntf, substance, 'NH2-terminal fragment').
wdef(p70s6k, protein, p70s6k).
wdef(p78s6k, protein, p78s6k).
wdef(parp,protein, 'poly(ADP-ribose)polymerase').
wdef(pdkl, protein, 'PDKl').
wdef (peptides, protein, peptide).
wdef(pkb, protein, 'PKB').
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phrase(t, cell, [t,'-',dr7], 't-DR7',r).
phrase(t, cell, [t,'-',drt,'/',b7,'-',1],'t-DR7/B7~1',r).
phrase(t, cell, [t,cell], 'T cell',r).
phrase(t, cell, [t,cells], 'T cell',r).
phrase(t, complex,[t,'-',cell,receptor],'T-cell receptor',r).
phrase(t,cell,[t,'-',dr7, cells],'t-DR7 cells',r).
phrase(t,cell,[t,'-',dr7,'/',b7,'-',1], 't-DR7/B7-1',r).
phrase(t,complex,[t,'-',cell,antigen,receptor],'T-cell antigen red
eptor',r).
phrase(threonine, aminoacid, [threonine, 229], 'threonine 229', r)
phrase(transcription, protein, [transcription, factor], 'transcript
ion factor', r).
phrase(trypan, smallmolecule, 'trypan blue', r).
phrase(wt, protein, [wt, akt], 'WT Akt', r).
phrase(zap, protein, [zap,'-',70],'ZAP-70',r).
phrase(zdevd, smallmolecule, [zdevd, '-', fmk], 'zDEVD-fmk', r).
phrase(il, protein,[il,'-',3],' interleukin-3',r).
wdef(ab, complex, antibody).
wdef(actin, protein, actin).
wdef(activated, state, active).
wdef(active, state, active).
wdef(ad, disease, 'Alzheimer''''s disease').
wdef(agc,protein, 'AGC').
wdef(akt, protein, 'AKT').
wdef (anergic, state, inactive).
wdef (anergic, state, inactive).
wdef (anergy, state, inactive).
wdef(antibody,complex,antibody).
wdef(antigen, substance, antigen).
wdef(aop, protein, 'Aop').
wdef(apoptosis, process, apoptosis).
wdef(bad, protein, 'BAD').
wdef(c3g, protein, 'C3G').
wdef('ca2+', smallmolecule,'Ca2+').
wdef(cas, protein, 'Cas').
wdef(caspase, protein, caspase).
wdef(caspase, protein, caspase).
wdef(cbl, protein, 'Cbl').
wdef(ccrsrh,protein,'CCRSrh').
wdef(cd28, protein, 'CD28').
wdef(cells, structure, cell).
wdef(cholesterol, smallmolecule, cholesterol).
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phosphorylate,r). phrase (phosphatidylinositol, smallmolecule, [phosphatidylinositol, 1 ,',',4,',',5,'-',triphosphate], 'phosphatidylinositol 1,4,5-tripho sphate',r). phrase (phosphoinositide, protein, [phosphoinositide, '-', dependent, protein, kinase], 'PDK1',r). phrase(phospholipase, protein, [phospholipase,c,'-',1],'phospholip ase C-1', r). phrase(poly,protein,[poly,'(',adp,'-',ribose,')',polymerase],'poly (ADP-ribose) polymerase',r). phrase (polyvinylidene, structure, [polyvinylidene, difluoride, memb ranes], 'polyvinylidene difluoride membranes', r). phrase(presenilin, protein, [presenilin, 1], 'presenilin 1', r). phrase(presenilin,protein,[presenilin,2],'presenilin,2',r). phrase(productively, state,[productively,stimulated],active,r). phrase(protein, protein, [protein,tyrosine,kinase],'protein tyrosi ne kinase', r). phrase(protein, protein, [protein, kinase, c], 'protein kinase C', r). phrase(ps2, substance, [ps2, '-', ctf], 'presenilin 2 COOH-terminal fra phrase(ps2, substance, [ps2, cleavage, fragment], 'presenilin 2 cleava ge fragment', r). phrase(pvdf, structure, [pvdf, membranes], polyvinylidene difluori de membranes', r). phrase(raf, protein, [raf,'-',1], 'Raf-1', r). phrase(raf,protein,[raf,'-',1], 'Raf-1',r). phrase(rap1,complex,[rap1,'-',gtp], 'Rap1-GTP',r). phrase (requirement, need2, [requirement, for], need,r). phrase(ser, smallmolecule, [ser, 19], 'Ser 19',r). phrase(ser, smallmolecule, [ser, 23], 'Ser 23',r). phrase(serine, substance, [serine, residues], 'serine residues', r phrase(src, domain, [src, homology, 2], 'Src homology 2',r). phrase(src, domain, [src, homology, 3], 'Src homology 3',r). phrase(srebp,protein,[srebp,'-',1], 'sterol-regulatory element bin ding protein 1',r). phrase(srebp,protein,[srebp,'-',2], 'sterol-regulatory element bin ding protein 2',r). phrase(sterol, protein, [sterol, '-', regulatory, element, binding, prote in,1],'sterol-regulatory element binding protein 1',r).

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phrase(sterol, protein, [sterol, '-', regulatory, element, binding, prote

in,2],'sterol-regulatory element binding protein 2',r).



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phrase(ice,protein, [ice,'/',ced,'-',3],'ICE/Ced-3',r).
phrase(il, gene, [il,'-',2,gene], 'gene encoding interleukin-2', r
) .
phrase(il, protein, [il,'-',2], 'interleukin-2',r).
phrase(in, interm, [in, the, case, of],[], r).
phrase(in, state, [in, the, anergic, state], inactive, r).
phrase(inducible, cell, [inducible,h4,cell], 'inducible H4 cell',r
) .
phrase(interleukin, protein, [interleukin,'-',2],r).
phrase(interleukin, protein, [interleukin, '-', 3], 'interleukin-3
',r).
phrase (interleukin, protein, [interleukin, '-',1, beta, converting, enzy
me], 'interleukin-1 beta converting enzyme',r).
phrase(jurkat, cell, [jurkat, cell], 'Jurkat cell', r).
phrase(jurkat, cell, [jurkat, cells], 'Jurkat cell', r).
phrase(kif3a,protein,[kif3a,'/',3,b],'KIF3A/3B',r).
phrase(lbl, cell, [lbl,'-',drf, cells], 'LBL-DR7 cells',r).
phrase(lbl,cell,[lbl,'-',dr7,cells],'LBL-DR7 cells',r).
phrase(let, protein, [let,'-',23], 'Let-23', r).
phrase(may, probability, [may, be], possible, r).
phrase(myc, protein, [myc, '-', p70s6kd3e], 'Myc-p70s6kD3E',r).
phrase(myc, protein, [myc, '-', pdk1], 'Myc-PDK1',r).
phrase(myc,protein,[myc,'-',p70s6k],'Myc-p70s6k',r).
phrase(myc,protein,[myc,'-',p70s6ke389d3e], 'Myc-p70s6kE389D3E',r)
phrase(myr, protein, [myr, '-', akt], 'Myr-Akt', r).
phrase(n,protein, [n,'-',methyl,'-',d,'-',aspartate, receptor], 'N
MDAR', r).
phrase(n,protein, [n,'-',methyl,'-',d,'-',aspartate], 'NMDA').
phrase(native, cell, [native, h4, cell], 'native H4 cell',r).
phrase(nf, protein, [nf,'-','[',kappa,']',b], 'NF-[kappa]B',r).
phrase(nh2, site, [nh2,'-',terminal], 'NH2-terminal',r).
phrase(nh2, substance, [nh2, '-', terminal, fragment], 'NH2-terminal fr
agment',r).
phrase(nih, cell, [nih, '-', 3, t3, fibroblasts], 'NIH-3T3 fibroblasts'
phrase(nih,cell,[nih,'-','3t3', fibroblasts],'NIH-3T3 fibroblasts'
phrase(normal, substance, [normal, ntf], 'normal NTF', r).
phrase(nuclear, protein, [nuclear, factor, kappa, b], 'NF-[kappa]B'
phrase(p150Glued,protein,[p150Glued,-,arp1],'p150Glued-Arp1',r).
phrase(phosphate,phosphorylate2, [phosphate, incorporated, into],
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phrase(caspase, protein, [caspase, '-', 6], 'caspase-6', r).
phrase(caspase,protein,[caspase,'-',7],'caspase-7',r).
phrase(catalytic, domain, [catalytic, domain], 'catalytic domain',
r).
phrase(cleavage,site,[cleavage,site],'cleavage site',r).
phrase(cleavage, substance, [cleavage, products], 'cleavage products',
phrase(cooh, substance, [cooh, '-', terminal, fragment], 'COOH-termina
l fragment',r).
phrase(crk,protein,[crk,proteins], 'crk proteins',r0.
phrase(crkl, complex,[crkl,'-',c3g,complex],'crkl-c3g complex',r).
phrase(dcp,protein,[dcp,-,1],'DCP-1',r).
phrase(did, negation, [did, not], not, r).
phrase (ebv, species, 'Epstein-Barr virus', r).
phrase(epstein, species, [epstein,'-',barr,virus],'Epstein-Barr vi
rus',r).
phrase(familial, disease, [familial, alzheimer, '''', s, disease], 'famil
ial Alzheimer'''s disease',r).
phrase(gene, gene, [gene,encoding,interleukin,'-',2],'gene encodin
g interleukin-2', r).
phrase(gst, protein, [gst,'-','fyn','-',sh2], 'GST-Fyn-SH2',r).
phrase(gst, protein, [gst,'-','fyn','-',sh3], 'GST-Fyn-SH3',r).
phrase(gtp, complex,[gtp,exchange,of,rapl],'GTP exchange of Rapl',
r).
phrase (guanidine, protein, [guanidine, nucleotide, '-', releasing, fac
tor, c3g], 'guanidine nucleotide-releasing factor C3G', r).
phrase(guanidine, smallmolecule, [guanidine, nucleotide], 'guanidine
nucleotide',r).
phrase (guanosine, smallmolecule, [guanosine, triphosphate], 'guanosin
e triphosphate',r).
phrase (guanosine, smallmolecule, [guanosine, diphosphate], 'guanosine
diphosphate',r).
phrase(h4,cell,[h4,cell,line], 'H4 cell line',r).
phrase(h4,cell,[h4,human,neuroglioma,cells], 'H4,human,neuroglioma
,cells',r).
phrase(ha, protein, [ha, '-', '[',delta,']',phpkb],'HA-[Delta]PHPK
B',r).
phrase(hla, protein, [hla,'-',dr7], 'HLA-DR7',r).
phrase(i, protein, [i, '[',kappa, ']',b,'-','[',beta,']'],
                                                               'I[ka
ppa]B-[beta]',r).
phrase(i,protein, [i, '[',kappa, ']',b,'-','[',alpha,']'], 'I[kap
pa]B-[alpha]',r).
phrase(i,protein, [i, '[',kappa, ']',b], 'I[kappa]B',r).
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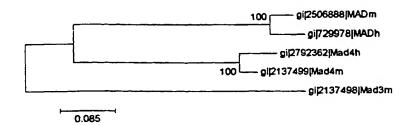
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% lexsemsub.pat
% revised March 17, 2000
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phrase('[',smallmolecule, ['[',zeta,']',1, subunit], '[zeta]1 subu
nit', r). % ?
phrase(116, protein,[116,'-',kd,fyn,'-',associated,protein],'116-k
D Fyn-associated protein',r).
phrase(116, protein,[116,'-',kd,protein], '116-kd protein',r).
phrase(3,protein, [3,'~',kinase,'-',akt], '3-kinase-Akt',r).
phrase(ability, affirmation, [ability, to], [], r).
phrase(agc, protein, [agc, protein, kinases], 'AGC', r).
phrase(akt, protein, [akt, mutant], 'Akt mutant', r).
phrase(alternative, substance, [alternative, ntf], 'alternative NTF', r
phrase(antibody, protein, [antibody, to, phosphotyrosine], 'anti-phosp
hotyrosine',r). .
phrase(antigen, complex, [antigen, receptor], 'antigen receptor',r).
phrase(ap, protein, [ap,'-',1],'AP-1',r).
phrase (aspargine, site, [aspargine, '-', 141], 'aspargine-141', r).
phrase(b, cell, [b,cell], 'B cell', r).
phrase(b, cell, [b,cells], 'B cell', r).
phrase(b, species, [b,lymphoblastoid,cells], 'B lymphoblastoid cell
s',r).
phrase(b,cell,[b,lymphoblastoid,cells], 'B lymphoblastoid cells',r
phrase(b7, protein, [b7,'-','1'], 'B7-1',r).
phrase(bcl,protein,[bcl,'-',2],'Bcl-2',r).
phrase(c, protein, [c,'-',jun] , 'c-Jun',r).
phrase(camk, protein, [camk, iv], 'CaMK IV',r).
phrase(casp, protein, [casp, '-', 3], 'caspase-3', r).
phrase(caspase, protein, [caspase, '-', 3, family, protease], 'caspase-3
 family protease',r).
phrase(caspase,protein,[caspase,'-',3,precursor],'caspase-3 precur
phrase(caspase,protein,[caspase,'-',3],'caspase-3',r).
phrase(caspase, protein, [caspase, -, 3], 'caspase-3', r).
```

Appendix A

Page 1

Α.



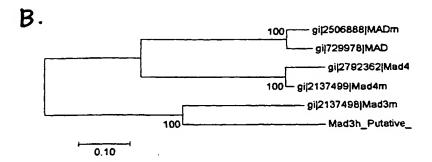


Figure 18. A-B

C

>Mad3h(Putative)

MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGPIHRRKKRPPQAPGAQDSGRSVHNELEKRRRAQLK RCLERLKQQMPLGGDCARYTTLSLLRRARMHIQKLEDQEQRARQLKERLRTKQQSLQRXWMQLRGLAGAAERER LRADSLDSSGLSSERSDSDOEELEVDVESLVFGGEAELLRGFVAGOEHSYSHVGGAWL

D

gi12506888[HADb gi17299781HADh gi12792362[Hadéh gi12137499[Hadéh gi12137498[Hadéh Hadéh Putative	MATAVOHRI OLLLEANDYLERRERLEHGYASHLPYS-KURDAFKRUKKPKORISTSSRSTHMEHEKKRAAHLRUCLEKLKGUVPLGPESSRRTTLSL; MAANWRITGILLEANDYLERRERLEHGYASHLPYNOGORDALKRUKSKORNIS-SSRSTHMEHEKRAAKLRULEHLKGUVPLGPESSRRTTLSL;HEINSLLILLEANEYLERDRELEHGYASVLPFODDFARIKKKANGUVRUAPNNESSHRELEKRHAKLRULTLGUKQULPVGPDSTRRTTLSL;HEINSLLILLEANEYLERRORLEHGYASVLPFODDFARIKKKANGUVRUAPNNESSHRELEKRHAKLRULTLGUKQULPDFLPDSTRRTTLSL;HEINSLLILLEANEYLERRORLEHGYASHLPFODDFARIGKTAGUVRUGPNNESSHRELEKRHAKLRULTLGUKQULPDFLPDSTRRTTLSL;HEPVASHIGYLLDANEFLERRERLEHGYASLCPHRSFGPIHRRKKRPPQAFGAGOSGRSVHHELEKRRAQUKRCLERLKQOHPLGGDCARYTTLSL;HEPVASHIGYLLDANEFLERRERLEHGYASLCPHRSFGPIHRRKKRPPQAFGAGOSGRSVHHELEKRRAQUKRCLERLKQOHPLGGDCARYTTLSL;
gil25068881MADm gil7299781MADb gil27923621Mad4h gil21374991Mad4m gil21374981Mad3m Mad3h Putative	TKAKLHI IKILEDCORKAVHOI DOLQREGREUKRULEKIGAFRTRHDSVG-SVVSSERSDSDREELDVDVDVDVDVDVDGTDYLMGDLGMSSS- TKAKLHI IKILEDCORKAVHOI DOLDREGREUKRIGE IRFA
gi125068881MADm gi77299781PADh gi127923621Mad4h gi127374991Mad4m gi121374981Mad3m Mad3h Putative	VSDSDERGSHOS LG-SDEGYSSAT-KRAKLODGHCGGG VSDSDERGSHOS LG-SDEGYSSTSHREIKLOGSBCGGG SSDADOHYSLOS GGGGDSSGFOPHCRILEGHALS SSDADOHYSLOS GGSDSS YGHPCRIPGCPGLS SDAGREIKSYSRSTGAML

Figure 17 C-D

BASE COUNT 130 a 234 c 258 g 106 t 5 others ORIGIN 1 cagcogottg ctccggccgg caccotaggc cgcagtccgc caggotgtcg ccgacatgga 61 accettggcc agcaacatcc aggtectgct geaggeggce gagtteetgg agegeegtga 121 gagagaggcc gagcatggtt atgcgtccct gtgcccgcat cgcagtccag gccccatcca 181 caggaggaag aagcgacccc cccaggctcc tggcgcgcag gacagcgggc ggtcagtgca 241 caatgaactg gagaagcgca ggagggccca gttgaagcgg tgcctggagc ggctgaagca 301 gcagatgeec ctgggeggeg actgtgeecg gtacaccaeg ctgageetge tgegeegtge 361 caggatgcac atccagaagc tggaggatca ggagcagcgg gcccgacagc tcaaggagag 421 gctgcgcaca aagcagcaga gcctgcagcg gcantggatg cagctccggg ggctggcagg 481 ngcggccgag cgggagcgnc tgcgggcgga cagtctggac tcctcaggcc tctcctctga 541 gcgctcagac tcagaccaag aggagctgga ggtggatgtg gagagcctgg tgtttggggg 601 tgaggccgag ctgctgcggg gcttcgtcgc cggccaggag cacagctact cgcacgtcgg 661 cggcgcctgg ctatgatgtt cctcacccan ggcgggcctc tgccctctta ctcqttgccc 721 aagcccactt tnc

Figure 17B

TBLASTK 2.0.8 [Jan-05-1999]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

Query= gi:|2137498|Mad3m (205 letters)

gb|AA278224|AA278224 zs77e05.rl NCI_CGAP_GCBl Homo sapiens cDNA clone IMAGE:703520 5' similar to TR:Gl184157 Gl184157 MAX-INTERACTING TRANSCRIPTIONAL REPRESSOR.; Length = 430

Score = 209 bits (526), Expect = 1e-53 Identities = 104/124 (836), Positives = 116/124 (92%), Gaps = 1/124 (0%) Frame = +2

Ouery: 1 MEPVASNIQVLLQAAEFLERREREAEHGYASLCPHHSPGTVCRRRKPPLQAPGALNSGRS 60 MEP+ASNIQVLLQAAEFLERREREAEHGYASLCPH SPG + RR+K P QAPGA +SGRS Sbjct: 56 MEPLASNIQVLLQAAEFLERREREAEHGYASLCPHRSPGPIHRRKKRPPQAPGAQDSGRS 235

Query: 61 VHNELEKRRRAQLKRCLEQLRQOMPLGVDCTRYTTLSLL-RARVHIQKLEEQEQQARRLK 119
VHNELEKRRRAQLKRCLE+L+QQMPLG DC RYTTLSLL RAR+HIQKLE+QEQ+AR+LK

Sbjct: 236 VHNELEKRRRAQLKRCLERLKQQMPLGGDCARYTTLSLLRRAAMHIQKLEDQEQRARQLK 415

Query: 120 EKLRS 124 E+LR+ Sbjct: 416 ERLRT 430

dbj:C02407:C02407 HUMGS0012279, Human Gene Signature, 3'-directed cDNA sequence. Length = 348

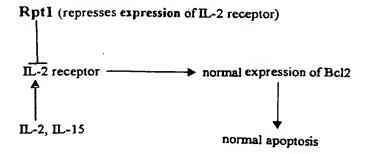
Score = 97.5 bits (239), Expect = 6e-20 Identities = 51/63 (80%), Positives = 56/63 (87%) Frame = +3

Query: 125 KQQSLQQQLEQLQGLPGARERERLRADSLDSSGLSSERSDSDQEDLEVDVENLVFGTETE 184 KQQSLQ+ Ql+GL GA ERERLRADSLDSSGLSSERSDSDQE+LEVDVE+LVFG E E Sbjct: 45 KQQSLQRXWMQLRGLAGAAERERLRADSLDSSGLSSERSDSDQEELEVDVESLVFGGEAE 224

Query: 185 LLQ 187 LL+ Sbjct: 225 LLR 233

Figure 17 A

Activated CD4⁺ T-cells



When rpt1 is knocked out:

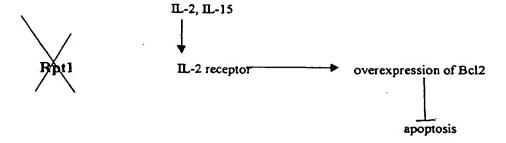


Figure 16

>sp|P15533|RPT1_MOUSE DOWN REGULATORY PROTEIN
OF INTERLEUKIN 2 RECEPTOR (J03776) rpt-lr [Mus
musculus] Length = 353

Score = 92.0 bits (237), Expect = 6e-20

```
Query 194 VMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILEGSVRNSMWRPAPFKCPTCRK 373
V+E+++E++TCPIC L +P C+H+FC+ C+ B S RN+ CP CR
Sbjct 5 VLEMIKEEVTCPICLELLKEPVSADCNHSFCRACITLNYE-SNRNT---DGKGNCPVCRV 60

Query 374 ETSATGINSLQVNYSLKGIVEKYNKIKISP----KMPVCKGHMGQPLNIFCLTDMQLICG 541
+L+ N + IVE+ K P K+ +C H G+ L +FC DM +IC
Sbjct 61 PYP---FGNLRPNLHVANIVERLKGFKSIPEEEQKVNICAQH-GEKLRLFCRKDMMVICW 116

Query 542 ICATRGEHTKHVFCSIEDAYAQERDAFESLFQSF------ETWRRGDALSRLDTMETSK 700
+C EH H IE+ +++ + W+ L R+D

Sbjct 117 LCERSQEHRGHQTALIEEVDQEYKEKLQGALWKLMKKAKICDEWQDDLQLQRVDW----- 171

Query 701 RKSLQLMTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMKLAVMQAYDPEINKL 862
+Q+ + + V+ F+ L+ LD K+NE L + K VM+ + N+L

Sbjct 172 ENQIQI---NVENVQRQFKGLRDLLDSKENEELQKLKKEKKEVMEKLEESENEL 222
```

Homology covers ring finger, B-box and the beginning of coiled coil domain in the CLL ring finger protein

Figure 15

10 15 20 25 30

1 S R S X Q K F F Q E L S K S L D A F P E D F C R H K V L P Q

31 L L T A F E F G N A G A V V L T P L F K V G K F L S A E E Y

61 Q Q K I I P V V V K M F S S T D R A M R I R L L Q Q M E Q F

91 I Q Y L D E P T V N T Q I F P H V V H G F L D T N P A I R E

121 Q T V K S M L L L A P K L N E A N L N V E L M K H F A R L Q

151 A K D E Q G P I R C N T T V C L G K I G S Y L S A S T R H R

181 V L T S A F S R A T R D P F A P S R V A G V L G F A A T H N

211 L Y S M N D C A Q K I L P V L C G L T V D P E K S V R D Q A

241 F K A X R S F L S K L E S V S E D P T Q L E E V E K D V H A

271 A S S P G M G G A A A S W A G W A

Figure 14D

BASE COUNT

405 a

545 c

278 t

6 others

```
ORIGIN
       1 cagoogaage amgcaaaaat tottocagga gotgagcaag agootggacg cattocotga
      61 qgayttctgt cggcacaagg tgctgccca gctgctgacc gccttcgagt tcggcaatgc
      121 tqqqqccgtt gtcctcacqc ccctcttcaa qqtqqqcaag ttcctgagcg ctgaggagta
      181 tcagcagaag atcatccctg tggtggtcaa gatgttctca tccactgacc gggccatgcg
     241 catccgcctc ctgcagcaga tggagcagtt catccagtac cttgacgagc caacagtcaa
     301 caccagate tteccecaeg tegtacatgg ettectggae accaaecetg ccateeggga
     361 qcaqacggtc aagtccatgc tgctcctggc cccaaagctg aacgaggcca acctcaatgt
     421 qqaqctqatg aagcactttg cacqqctaca qqccaaggat gaacagggcc ccatccgctg
     481 caacaccaca gtctgcctgg gcaaaatcgg ctcctacctc agtgctagca ccagacacag
     541 ggtccttacc tctgccttca gccgagccac tagggacccg tttgcaccgt cccgggttgc
      601 qqqtqtcctg ggctttqctq ccaccacaa cctctactca atgaacgact gtgcccagaa
     661 gatectqcct qtqctctqcq qtctcactqt aqatectqag aaatccgtgc gagaccaggc
     721 cttcaaggcm wttcggagct tcctgtccaa attggagtct gtgtcggagg acccgaccca
     781 gctggaggaa gtggagaagg atgtccatgc agcctccagc cctggcatgg gaggagccgc
     841 agctagctgg gcaggctggg cgtgaccggg gtctcctcac tcacctccaa gctgatccgt
     901 tegeacecaa ecaetgeece aacagaaace aacatteece aaagacecae geetgaagga
     961 gttcctgccc cagcccccac ccctgttcct gccaccccta caacctcagg ccactgggag
    1021 acgcaggagg aggacaagga cacagcagag gacagcagca ctgctgacag atgggacgac
    1081 gaagactggg gcagcctgga gcaggaggcc gagtctgtgc tggcccagca ggacgactgg
    1141 agcaccgggg gccaagtgag ccgtgctagt caggtcagca actccgacca caaatcctcc
    1201 aaatccccag agtccgactg gagcagctgg gaarctgagg gctcctggga acagggctgg
    1261 caggagccaa gctcccagga gccacctyct gacggtacac ggctggccag cgagtataac
    1321 tggggtggcc cagagtccag cgacaagggc gacccettcg ctaccetgte tgcacgtccc
    1381 agcacccagc cgaggccaga ctcttggggt gaggacaact gggagggcct cgagactgac
    1441 agtcgacagg tcaaggctga gctggcccgg aagaagcgcg aggagcggcg gcgggagatg
     1501 gaggccaaac gcgccgagag gaaggtgcca agggccccat gaagctggga gcccggaagc
     1561 togactgaac cotogoogto occettocoo octocogaga occooccoa cagatotatt
     1621 tattqtacaa accatgtgag cccqqccqcc caqccaggcc atctcacgtg tacataatca
     1681 gagccacaat aaattctatt tcacaaaaaa aaaaaaaaa aaaaaaa
1.1
```

493 g

Figure 14C

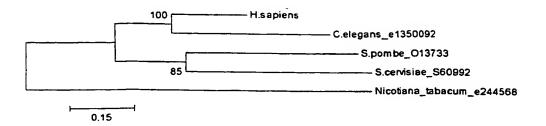


Figure 14B

>gi||34'9211|gb|W51957|W51957 zc45f01.rl Soares_senescent_fibroblasts_NbHSF Homo
sapiens cDNA clone IMAGE:325273 5', mRNA sequence [Homo sapiens]
CCTTCGAGTTCGGCAATGCTGGGGCCGTTGTCCTCACGCCCCTCTTCAAGGTGGGCAAGTTCCTGAGCGC
TGAGGAGTATCAGCAGAAGATCATCCCTGTGGTGGTCAAGATGTTCTATCCACTGACCGGGCCATGCGC
ATCCGNCTCCTGCAGCAGATGGAGCAGTTCATCCAGTACCTTGACGAGCCAACAGTCAACACCCAGATCT
TCCCCCACGTCGTACATGGCTTCCTGGACACCCAACCCTGCCATCCGGGAGCAGACGGTCAAGTCCATGCT
GCTCCTGGCCCCAAAGCTGAACGAGGCCAACCTCAATGTGGAGCTGATGAAGAACTTTGCACGGCTACAG
GCCAAGGATGAACAGGGCCCCATCCGCTGCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCA
GTGCTAGCACCAGACACAGGGTCCTTACCTCTG

Figure 14A

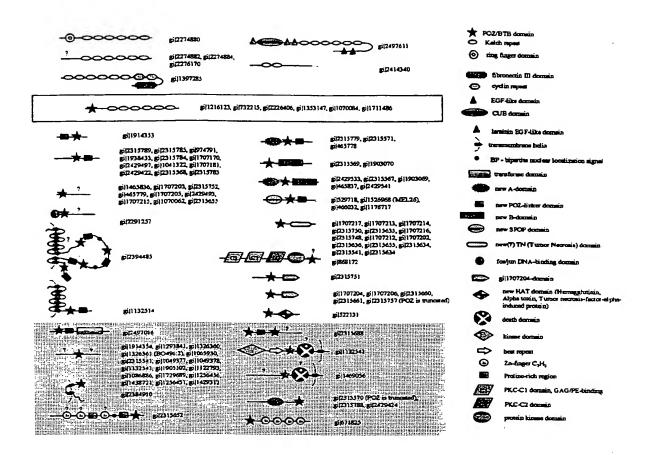


Figure 13

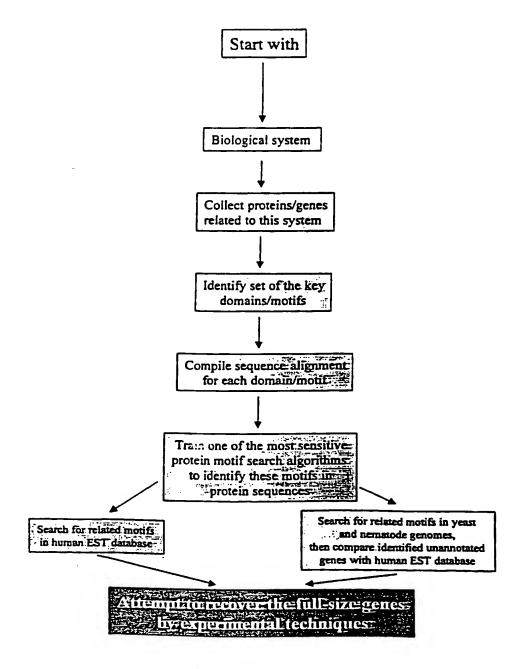


FIGURE 12

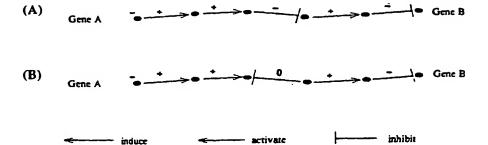


FIGURE 11

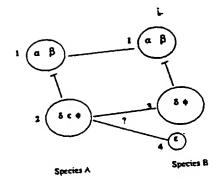


FIGURE 10

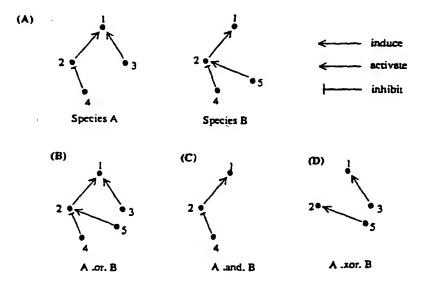


FIGURE 9

FIGURE 8

Start with Start with Start with a single Biological system a single gene a gene family Reconstruct a "network" of interacting genes and proteins Identify a set of key domains and motifs Search for related motifs in databases of known organisms Identify members of multigene families Compute phylogenetic trees Paralogous neworks Identify clusters of paralogous genes, identify paralogous and orthologous Herworks Paralogous networks in human

Compare regulatory schemes, identify genes that are known in one but missing in another system.

Find the genes using experimental techniques.

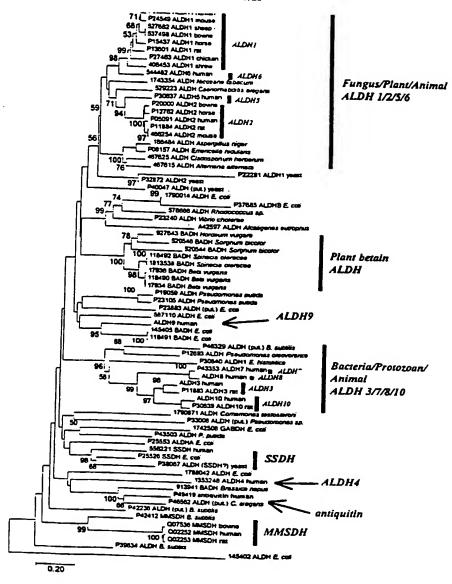


FIGURE ?

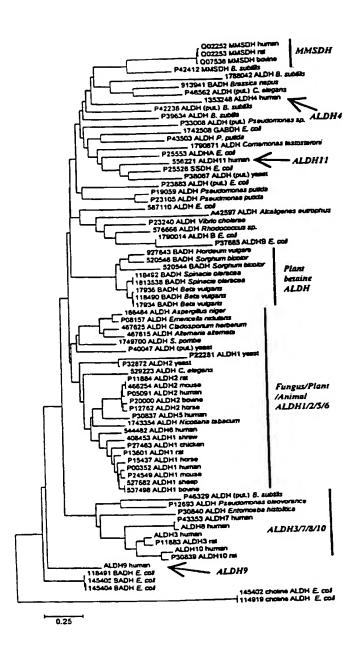


FIGURE 6

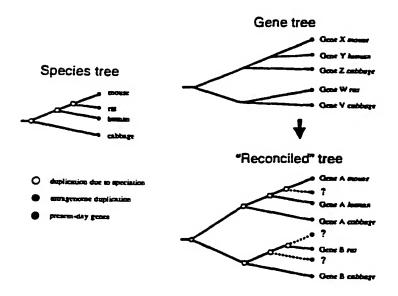
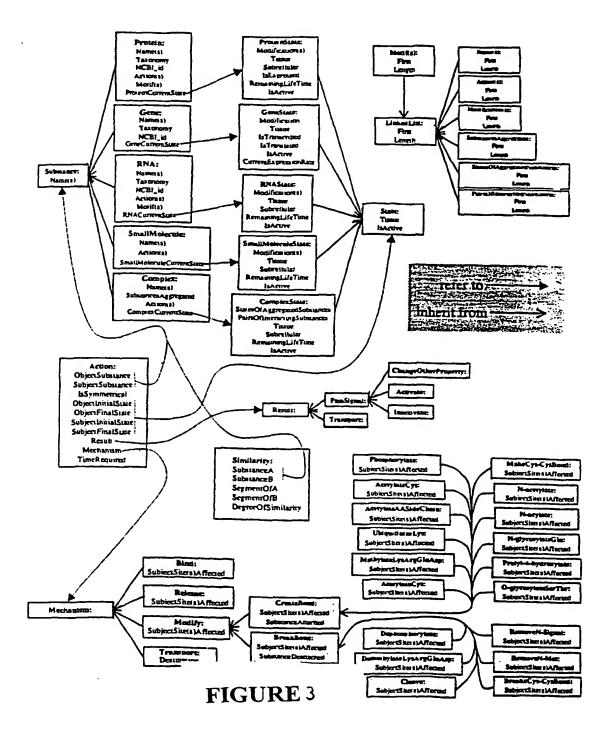


FIGURE 5

FIGURE 4

bd:-zL/ bd / bd:-xS/ ced-9/ Bax / BBx / BBx / p21 / NGFI-B / N10 / Nak1 / Nmr77 / Nurri / Nor-1 / Not-1 / RXR / galectin-1 / N-glycan / CNTF / lck / fyn / ZAP-70 / raf / ras / MAP / protein kinser C / PEC / phosphatase calcinents / NF-AT / AP1 / 14-3-3 / Raf-1 / Bcl-2 / Interteukts / IL-1 / IL-3 / cytokine / IGF-1 / CD95 / Apo-1 / RIP / FAF1 / FADD / FAP-1 / TNFF / TRAF1 / TRAF1 / TRAP1 / TRAP2 / TRADD / HIAP1 / HIAP2 / CD40 / CD30 / XIAP / CD2 / CD3 / TCR / Bcl-w / Mcl-1 / NR-13 / BHRF1 / HMWS-EL / E1B19K / Nbk / Mch2 / CPF-22 / ICE / FLICE / Nedd-2 / TX / Mch3 / Mch4 / ICB-1s / Interteukts / DNAsel / caspase / MACB1 / Mch5 / apopain / Yams / ICB / CMB / ced-3 / ced-4 / ced-9 / p53 / MKE3 / MKE4 / MKE4 / MKE4 / BAG-1 / Src / FAST / p38 / p42 / ERK1 / p44 / ERK2 / SAPE / JNE / MEE / C-JUN / MEE F2D / ATF2 / calcineum / ELK-1 / protein phosphatase 2A / raf-1 / IL-1 brts / TNF / FTK / Apsf / p35 / ETS / C-Myc / IL-2 / IL-2 receptor / NF-kappa B / TNFR-1 / TRAIL / Apo-2L / DR4 / death receptor / DR3 / DR2 / DR3 / DR1 / bnd / BMP-x / TGF / grim / bid / FAN / perforin / Fas-L / Fas / DcR1 / decoy receptor / wsi-1 / NGF receptor / growth factor / RAF



3/23

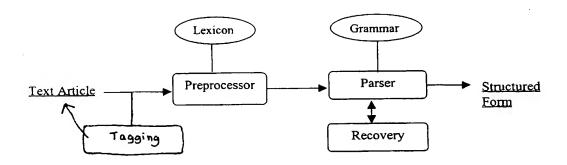


Figure 2

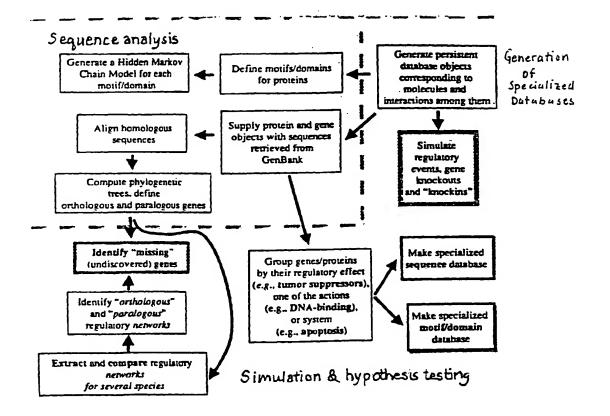


FIGURE 1

31. The system according to claim 22, wherein said error recovery means comprises:

means for segmenting the text data; and
means for analyzing the segmented text data to achieve at least a partial
parsing of the unsuccessfully parsed text data.

32. The system according to claim 22, wherein said tagging means comprises means for providing the structured data component in a Standard Generalized Markup Language (SGML) compatible format.

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phrases.

further comprises:

- 24. The system according to claim 22, further comprising means for referring to an additional parameter which is indicative of the degree to which subphrase parsing is to be carried out.
- The system according to claim 22, wherein said parsing meansfurther comprises means for segmenting the text data by sentences.
 - 26. The system according to claim 22, wherein said parsing means further comprises:

means for segmenting the text data by sentences; and means for segmenting each of the sentences at identified words or

27. The system according to claim 22, wherein said parsing means

means for segmenting the text data by sentences; and means for segmenting each of the sentences at a prefix.

- 15 28. The system according to claim 22, wherein said parsing means further comprises means for skipping undefined words.
 - 29. The system according to claim 22, wherein said parsing means further comprises:

means for identifying one or more binary actions and their relationships;

20 and

means for identifying one or more arguments associated with the actions.

30. The system according to claim 22, further comprising means for performing error recovery when parsing of the text data is unsuccessful.

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- 17. The method according to claim 11, wherein said parsing step further comprises skipping undefined words.
- 18. The method according to claim 11, wherein said parsing step further comprises:

identifying one or more binary actions and their relationships; and identifying one or more arguments associated with the actions.

- 19. The method according to claim 11, further comprising performing error recovery when parsing of the text data is unsuccessful.
- The method according to claim 19, wherein said error recovery step comprises:

segmenting the text data; and

analyzing the segmented text data to achieve at least a partial parsing of the unsuccessfully parsed text data.

- 21. The method according to claim 11, wherein said tagging step

 comprises providing the structured data component in a Standard Generalized Markup

 Language (SGML) compatible format.
 - 22. A computer system for extracting information on biological entities from natural-language text data, comprising:
 - (i) means for parsing the natural-language text data; and
- 20 (ii) means for regularizing the parsed text data to form structured word terms.
- The system according to claim 22, further comprising means for preprocessing the data prior to parsing, with the preprocessing means comprising
 identifying biological entities.

10. The method of claim 9 further comprising using each identified expression sequence tag to search sequence databases for overlapping sequences for the purpose of assembling longer overlapping stretches of DNA.

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- 11. A method for extracting information on interactions between biological entities from natural-language text data, comprising:
 - (i) parsing the text data to determine the grammatical structure of the text data; and
 - (ii) regularizing the parsed text data to form structured word terms.
- 12. The method according to claim 11, further comprising preprocessing the data prior to parsing, with preprocessing comprising the step of identifying biological entities.
- The method according to claim 11, further comprising referring
 to an additional parameter which is indicative of the degree to which subphrase parsing is to be carried out.
 - 14. The method according to claim 11, wherein said parsing step further comprises segmenting the text data by sentences.
- The method according to claim 11, wherein said parsing step further comprises:

segmenting the text data by sentences; and segmenting each of the sentences at identified words or phrases.

- 16. The method according to claim 11, wherein said parsing step further comprises:
- 25 segmenting the text data by sentences; and segmenting each of the sentences at a prefix.

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- (v) imputing the species tree and gene tree into an algorithm which integrates the species tree and the gene tree into a reconciled tree; and
- (vi) identifying orthologous genes present in one species but missing in another.
- 8. The method of claim 7 wherein the following algorithm is used to integrate the species tree and the gene tree into a reconciled tree:
 - (i) computing the similarity $\sigma(S_{gi},S_{sj})$ for each pair of interior nodes from trees T_g and T_s ,
 - (ii) finding the maximum $\sigma(S_{gi},S_{si})$;
 - (iii) saving S_{gi} as a new cluster of orthologs, save $\{S_{gi}\}$ $\{S_{sj}\}$ as a set of species that are likely to have gene of this kind (or lost it in evolution);
 - (iv) eliminating S_{gi} from T_g ; T_g : = $T_g \setminus S_{gi}$;
 - (v) repeating step (ii)-(iv) until T_g is non-empty.
 - 9. A method for identifying a novel gene comprising the following steps:
 - defining a motif or domain composition of a gene of interest;
 - (ii) searching for sequences which correspond to nucleotide sequences in an expression sequence tag database or other cDNA databases using a program such as BLAST and retrieving the identified sequences;
 - (iii) searching additional databases for expressed sequence tags containing the domains and motifs characteristic for the gene of interest with Hidden Markov Model of domains and motifs identified in step (i);
 - (iv) identifying nucleotide sequences comprising the gene of interest.

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- The method of claim 1 wherein the regulatory pathway is involved 4. in apoptosis. The method of claim 1 wherein the specific protein from the first 5. species is involved in tumor suppression. 6. A method for identifying the affect of a gene knockout on a regulatory pathway comprising the following steps: (i) identification of the shortest non-oriented pathway connecting two gene products; assigning an initial sign value of "-" to the knockout since (ii) the knockout gene product is inactive; (iii) moving along the shortest pathway between the two gene products multiplying the sign with the sign of the next gene product in the pathway, wherein "-" stands for inhibition, "+" stands for induction or activation, and "0" stands for the lack of interaction between two proteins in the specified direction; and (iv) determining the final sign at the end of the pathway,
 - (iv) determining the final sign at the end of the pathway, wherein "-" indicates inhibition and "+" indicates induction or activation of the pathway.
 - 7. A method for identifying a novel nucleic acid molecule encoding a protein of interest comprising:
 - selecting a gene of interest and searching a database for homologous sequences;
 - (ii) aligning the homologous sequences identified in step (i);
 - (iii) constructing a gene tree using the sequence alignment;
 - (iv) constructing a species tree;

CLAIMS

A method for identifying a novel nucleic acid molecule encoding 1. a protein of interest comprising: selecting a specific protein from a first species involved (i) in a regulatory network of interest; 5 identifying known proteins that act upstream and (ii) downstream in the regulatory network of interest with respect to the specific protein selected; constructing the regulatory network of interest from the (iii) proteins identified in step (ii); 10 for each identified protein, select a domain or motif and (iv) search by homology for related proteins in a second species, wherein a related protein is defined as a protein having a homologous domain or motif; producing a regulatory network for the second species, (v) 15 wherein said regulatory network incorporates the identified related proteins; comparing the regulatory network from the first species to (vi) the regulatory network of said second species; identifying a protein present in a regulatory network for 20 (v) one species but absent in the regulatory network of the other species; and isolating a nucleic acid molecule encoding the protein (vi) identified in step (v) in the species in which it is missing. The method of Claim 1 wherein the nucleic acid molecule encodes 25 2. human protein.

The method of claim 1 wherein the related proteins are orthologs.

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WI). The nucleotide sequence of the human *Mad3* gene is presented in Figure 17B. The deduced amino acid sequence of the gene is presented in Figure 17C. The translated sequence consists of 206 amino acid residues 81% of which are identical to mouse Mad3 protein. The alignment of human and mouse Mad3 proteins shown below was made using BLAST server at NCBI and is presented in Figure 17C.

Multiple alignment of the new sequence with sequences of known Mad proteins was made using Clustalw and viewed with the HitViewer. A gene tree was computed from this alignment using NJBOOT. Multiple alignment of the new sequence with sequences of known Mad proteins (Figure 17C) along with its position on gene tree (Figure 18B) shows that this new human gene found by the approach described above belongs to the family of Mad proteins and is the ortholog of mouse Mad3.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

Various publications are cited herein, the contents of which are hereby incorporated by reference in their entireties.

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The gene tree shown in the Figure 20 was constructed in the following way. The protein sequences of known members of *Mad* gene family were extracted from GenBank database using NCBI Entrez keyword searches. The extracted sequences were aligned using multiple alignment program Clustalw running on Sun SPARC station. The quality of the multiple alignment was checked using program HitViewer Iterate (A. Rzhetsky, available upon request) and the redundant, non-homologous sequences as well as distant homologs from *S. cerevisiae*, *C. elegans*, *D. melanogaster* etc. were removed from the alignment. The refined set of sequences was realigned with Clustalw and a gene tree as presented in Figure 15A was computed from the alignment using program NJBOOT (http://genome6.cpmc.columbia.edu // andrey) running on Sun SPARC station and viewed with program TreeView (http://genome6.cpmc.columbia.edu // andrey).

The tree presented in Fig. 19A clearly shows the relationships between three known mouse genes and their two human homologs. Attempts to find a missing human ortholog of the mouse *Mad3* gene in protein non-redundant database at NCBI using BLAST search did not identify any human homologs other than sequences that were already present on the tree, confirming the absence of a known human ortholog for Mad3 protein in the database.

In order to identify a human ortholog of the Mad3 protein, a human dbEST at NCBI was searched with program TBLASTN using Mad3 protein sequence as a query. Two EST were identified and are shown in Figure 17A.

Due to the nature of dbEST database this search produced only partial sequences of potential candidate genes. To obtain complete coding sequences (complete cds) of the genes, a search was conducted to obtain overlapping sequences in dbEST. The search for overlapping sequences was performed using the program Iterate with EST zs77e55.r1 (gb|AA278224) serving as a query. The search returned a single overlapping sequence, namely HUMGS0012279 (dbj|C02407), thus indicating that the two EST sequences found during the initial TBLASTN search belong to the same gene.

The complete sequence of the gene was assembled from the two ESTs using commercially available sequence assembly program SeqManII (DNASTAR Inc.,

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sites and apparently antagonize *Myc*-mediated activation of the same set of target genes.

During tissue development a shift from Myc:Max to MAD:Max complexes occurs coincidentally with the switch from cell proliferation to differentiation. The switch in heterocomplexes is thought to reflect a switch from activation to repression of common genes leading to cessation of proliferation, exiting the cell cycle and the beginning of cell differentiation. In differentiating neurons, primary keratinocytes, myeloid cell lines and probably other tissues the expression of different MAD:Max complexes appear in sequential order during the transition from cell proliferation to differentiation. The MAD3 expression appears first and it is restricted to proliferating cells prior to differentiation where it is co-expressed with two different member of Myc family, c-Myc or N-Myc. Mxi1 transcripts are detected in proliferating and differentiating cells whereas MAD1 and MAD4 were confined to post-mitotic cells. Because Myc expression is not always downregulated in post-mitotic cells, co-expression of Myc and MAD genes may result in competition for Max heterodimers thus providing promoting or inhibitory effect on cell proliferation.

The gene expression patterns, along with ability of Mad proteins to suppress *Myc*-dependent transformation, are consistent with a potential function of Mad genes as tumor suppressors. This view is supported by the fact that allelic loss and mutations were detected at the *Mxi1* locus in prostate cancers (Eagle et al., 1995 Nat Genet 9:249-55). Cloning of the murine proteins *Mad3* and *Mad4* as well as their relation to *Max* signaling network was described by Hurlin (Hurlin PJ, et al., 1995, EMBO J. 14:5646-59) and Queva (Queva et al. 1998 Oncogene 16:967-977). Human orthologs of *Mad4*, *Mad1* and *Mxi1* are known.

In this example, the discovery of an unknown human ortholog of *Mad3* protein found "in silico," by means of phylogenetic analysis of known mouse and human members of the *Mad* gene family and database searches is described. Since the function of murine *Mad3* as a *Max*-interacting transcriptional repressor of *Myc*-induced neoplastic transformation is well described, we can assign the same

30 function to its human ortholog.

protein (sp|P15533|RPT1) (Figure 13). Analysis of regulatory functions of RPT1 in the mouse reveals that this gene functions as a repressor of the interleukin 2 receptor (IL-2R) gene. When the RPT1 gene is knocked out, the regulatory effect is manifested as a block of the apoptotic pathway in T lymphocytes resulting in an accumulation of T lymphocytes in blood. This result is consistent with aberrations observed in CLL, namely abnormal accumulation of B-cells in the blood (Trentin L. et al., 1997, Leuk. Lymphoma 27:35-42) and mutations in the human RPT1 gene play a role in development of CLL.

6.1.3 EXAMPLE: A DISCOVERY OF A HUMAN ORTHOLOG OF THE MURINE MAX-INTERACTING TRANSCRIPTIONAL

REPRESSOR

The family of *Myc* proto-oncogenes encodes a set of transcription factors implicated in regulation of cell proliferation, differentiation, transformation and apoptosis. *C-Myc* null mutations result in retarded growth and development of mouse embryos and are lethal by 9-10 day of gestation. In contrast, overexpression of *Myc* genes inhibits cell differentiation and leads to neoplastic transformation.

Moreover, deregulation of *Myc* expression by retroviral transduction, chromosomal translocation or gene amplification is linked to a broad range of naturally occurring tumors in humans and other species.

Another protein, called Max, is an obligatory heterodimeric partner for Myc proteins in mediating their function as activators of transcription during cell cycle progression, neoplastic transformation and programmed cell death (apoptosis). In order to make an active transcription factor the Myc proteins must form heterodimers with Max protein. This interaction with Max protein is necessary for specific binding of Myc with CACGTG box (or related E-boxes) on DNA and for activation of promoters located proximal to the binding sites.

Besides the *Myc* family of transcription factors, the *Max* protein forms complexes with another family of so-called *MAD* proteins: *Mxi1*, *MAD1*, *MAD3* and *MAD4*. Whereas *Myc:Max* complexes activate transcription, *MAD:Max* complexes work in an opposite way repressing the transcription through the same E-box binding

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The two closest human sequences, AA481214 and W51957, are depicted in Figure 14A. To determine whether the identified human sequences were orthologs or paralogs to the gi 1132541 gene of *C. elegans*, a gene tree (Saito and Nei, 1997, Molecular Biol. Evol. 4:406-425) was computed. The gene tree was generated using homologous genes identified with a BLASTP search against NCBI non-redundant database, using the human EST AA481214 sequence as a query. The resulting tree indicates that the identified human EST AA481214 represents a true ortholog of the *C. elegans* gene gi 1132541 (Figure 14B). The nucleotide sequence of the death domain protein is shown in Figure 14C, as well as the deduced amino acid sequence presented in Figure 14D.

6.1.2 APOPTOSIS GENE DISCOVERY METHOD

As a first step in identifying a novel gene involved in apoptosis, a comprehensive set of articles describing the system of apoptosis/programmed cell death in different species was compiled using the keyword "apoptosis". By analyzing the articles, information on regulatory pathways characterizing this system in different species, *i.e.*, *C. elegans*, mouse, fruit fly, chicken, and human, was extracted. The regulatory information was stored as a collection of schemes produced in PowerPoint (Microsoft). Figure 4 shows a set of keywords defining proteins involved in apoptosis pathways. The keywords were used to generate a specialized sequence database, referred to as Apoptosis3, utilizing the PsiRetriever program for extraction of proteins from the all-inclusive non-redundant GenBank database (NCBI). Using program PsiRetriever, sequences from the non-redundant (NCBI) database of protein sequences, were retrieved and stored as a FASTA file. The FASTA file was then converted into binary blast database using program FORMATDB from the BLAST suit of programs.

Genomic and cDNA sequences located in the region of human chromosome 13q were compared with the Apoptosis3 database using BLASTALL program from BLAST program complex. This region of the human genome is associated with Chronic Lymphocytic Leukemia (CLL). The comparison revealed significant similarity between a CLL region open reading frame and the mouse RPT1

groupings of proteins: (i) proteins known to be tumor suppressors, and (ii) proteins implicated in apoptosis in animals were developed.

6.1 APOPTOSIS GENE DISCOVERY METHOD

Identification of a putative apoptosis-related human gene began with an identification of all genes in *C. elegans* that contained either a POZ or kelch domain. A subset of these genes is shown in Figure 13. Hidden Markov Models (HMM) for the POZ and Kelch domains were built as follows. Starting with POZ and kelch sequences from the *Drosophilia* kelch protein (gi | 577275) homologs were identified in other protein sequences using the BLASTP program. The resulting sequences showing significant similarity (e-value less than 0.001) were aligned using CLUSTALW program and the alignments were used to build Hidden Markov Models with HMMER-2 package (Krogh et al., 1995, :http://hmmer.wustl.edu/). A computer printout listing of HMM models of tumor suppressors appears as a Microfiche H to the present specification. (See, http://hmmer.wustl.edu; Chapter 2, which is incorporated by reference herein in its entirety, for a detailed description of HMM models)

The resulting models were used to search through a database collection of *C.elegans* protein sequences. The domain structures of proteins having either a POZ or kelch domain were identified using existing collections of protein domains (e.g., see http://blocks.fhcrc.org/blocks/blocks release.html, http://coot.embl-heidelberg.de/SMART/, http://www.motif.genome.ad.jp/). One of the unannotated protein-coding genes of *C. elegans* (corresponding protein accession number gi | 1132541, see Figure 11) appeared to include a POZ domain, death domain, kinase domain, and heat repeat. A death domain is characteristic for the apoptosis system and a kinase domain indicates that the protein is likely to participate in phosphorylation of other proteins. The presence of these particular domains suggests that this protein is serving as a regulatory protein.

Using the protein sequence of gi 1132541, the database of human EST sequences was searched and a number of partial human cDNA sequences representing potential human orthologs or paralogs of the *C.elegans* gi 1132541 were identified.

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In another embodiment, polymerase chain reaction (PCR) can be used to amplify the desired sequence from a genomic or cDNA library. To isolate orthologous or paralogous genes from other species, one synthesizes several different degenerate primers, for use in PCR reactions. In a preferred aspect, the oligonucleotide primers represent at least part of the gene comprising known ortholog or paralog sequences of different species. It is also possible to vary the stringency of hybridization conditions used in priming the PCR reactions, to allow for greater or lesser degrees of nucleotide sequence similarity between the known nucleotide sequences and the nucleic acid homolog being isolated.

Synthetic oligonucleotides may be utilized as primers to amplify by PCR sequences from a source (RNA or DNA), preferably a cDNA library, of potential interest. PCR can be carried out, e.g., by use of a Perkin-Elmer Cetus thermal cycler and a thermostable polymerase, e.g., Amplitaq (Perkin-Elmer). The nucleic acids being amplified can include mRNA or cDNA or genomic DNA from any eukaryotic species. After successful amplification of a segment of a the gene of interest, that segment may be molecularly cloned and sequenced, and utilized as a probe to isolate a complete cDNA or genomic clone.

Once identified and isolated the gene of interest can then be inserted into an appropriate cloning vector for amplification and/or expression in a host. A large number of vector-host systems known in the art may be used. Possible vectors include, but are not limited to, plasmids and modified viruses, but the vector system must be compatible with the host cell used. Such vectors include, but are not limited to, bacteriophages such as lambda derivatives, or plasmids such as pBR322 or pUC plasmid derivatives or the Bluescript vector (Stratagene). The insertion into a cloning vector can, for example, be accomplished by ligating the DNA fragment into a cloning vector which has complementary cohesive termini.

6. EXAMPLE: USE OF SPECIALIZED DATABASES FOR IDENTIFICATION OF NOVEL GENES

To test the method of using databases for gene discovery, protein sequence and domain/motif databases specific to two overlapping functional

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carried out in the same solution with the following modifications: 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml salmon sperm DNA, 10% (wt/vol) dextran sulfate, and 5-20 X 106 cpm ³²P-labeled probe is used. Filters are incubated in hybridization mixture for 18-20 h at 40°C, and then washed for 1.5 h at 55°C in a solution containing 2X SSC, 25 mM Tris-HC1 (pH 7.4), 5 mM EDTA, and 0.1% SDS. The wash solution is replaced with fresh solution and incubated an additional 1.5 h at 60°C. Filters are blotted dry and exposed for autoradiography. If necessary, filters are washed for a third time at 65-68°C and reexposed to film. Other conditions of low stringency which may be used are well known in the art (e.g., as employed for cross species hybridizations).

In another specific embodiment, a nucleic acid which is hybridizable to a nucleic acid under conditions of moderate stringency is provided. For example, but not by way of limitation, procedures using such conditions of moderate stringency are as follows: filters containing DNA are pretreated for 6 h at 55°C in a solution containing 6X SSC, 5X Denhart's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA. Hybridizations are carried out in the same solution and 5-20 X 10⁶ CpM ³²P- labeled probe is used. Filters are incubated in the hybridization mixture for 18-20 h at 55°C, and then washed twice for 30 minutes at 60°C in a solution containing 1X SSC and 0.1% SDS. Filters are blotted dry and exposed for autoradiography. Other conditions of moderate stringency which may be used are well-known in the art. Washing of filters is done at 37°C for 1 h in a solution containing 2X SSC, 0.1% SDS.

For expression cloning (a technique commonly used in the art), an expression library is constructed. For example, mRNA is isolated from the cell type of interest, cDNA is made and ligated into an expression vector (e.g., a bacteriophage derivative) such that it is capable of being expressed by a host cell (e.g., a bacterium) into which it is then introduced. Various screening assays can then be used to select for the expressed gene product of interest based on the physical, chemical, or immunological properties of its expressed product. Such properties can be deduced from the properties of the corresponding orthologs from other species.

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knock out of gene A which can be any one of the following: inhibition of gene B, induction/activation of gene B, or none. In addition to the "electronic knock out", an "electronic knock in" of a particular gene can be simulated. In such a computer simulation, the artificial addition of a gene and its effect on a regulatory system may be analyzed.

5.6. <u>IDENTIFICATION AND ISOLATION OF NOVEL GENES</u>

The present invention relates to identification of novel genes, i.e., missing orthologs or paralogs, and the isolation of nucleic acid molecules encoding novel genes. In a specific embodiment, a nucleic acid molecule encoding a missing ortholog or paralog can be isolated using procedures well known to those skilled in the art (See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York Glover, D.M. (ed.), 1985, DNA Cloning: A Practical Approach MRL Press, Ltd., Oxford, U.K. Vol. I, II.).

For example, genomic and/or cDNA libraries may be screened with labeled DNA fragments derived from a known ortholog or paralog from a specific species and hybridized to the genomic or cDNA libraries generated from a different species. For cross species hybridization, low stringency conditions are preferred. For same species hybridization, moderately stringent conditions are preferred. Any eukaryotic cell potentially can serve as the nucleic acid source for the molecular cloning of the gene of interest. The DNA may be obtained by standard procedures known in the art from cloned DNA (e.g., a DNA "library"), by cDNA cloning, or by the cloning of genomic DNA, or fragments thereof, purified from the desired cell.

By way of example and not limitation, procedures using conditions of low stringency are as follows (see also Shilo and Weinberg, 1981, Proc. Natl. Acad. Sci. USA 78:6789-6792; and Sambrook et al. 1989, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring harbor, New York): Filters containing DNA are pretreated for 6 h at 40°C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HC1 (pH 7.5), 5 mM EDTA, 0.1% PVP, 0.1% Ficoll, 1% BSA, and 500 mg/ml denatured salmon sperm DNA. Hybridizations are

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while the "object" substance can be in either active, or inactive, state depending on the action type. For example, the action "dephosphorylation" requires an active phosphatase ("subject" substance) and a phosphorylated substitute protein ("object" substance) in phosphorylated form. If both conditions are satisfied, the action is recorded as in progress. At termination, the substances must change their states as specified by the action. On each following "quantum" of time, the simulation proceeds in the same way while maintaining the "bookkeeping" of the remaining time for each action and the remaining lifespan of each substance. The simulation stops when there are no more active actions available. The program allows editing of the properties of the objects, changing the scale and focus of the visualized simulation, and experimenting with the systems output.

In a specific embodiment of the invention a "knock out" of a gene can be simulated to model the regulatory system that normally includes hypothetical gene A. One of the typical questions related to the gene knock out is how does the knock out affect a biological pathway of interest. A hypothetical example of evaluating the impact of a knock out of hypothetical gene A on the expression of a hypothetical gene B is shown in Figure 12. The answer to such a question could be "gene B will be inhibited" or "gene B will be induced" or "no effect".

In the practice of the present invention, a simple algorithm involving multiplication of gene interaction "signs" along the shortest pathway between the genes can be used to determine the outcome. The algorithm involves the following steps: (i) identification of the shortest non-oriented pathway connecting genes A and B involved in a pathway of interest; (ii) assigning sign "-" to gene A since it is knocked out and taking this sign as the initial sign value; (iii) moving along the shortest pathway between genes A and B, multiplying the current value of the sign with the sign of the next arc, where "-" stands for inhibition, "+" stands for induction or activation, and "0" stands for the lack of interaction between two proteins in the specified direction; (iv) determining if the final result of multiplication is "0", if so eliminating the zero arc and trying to find the shortest oriented bypass pathway between A and B in the remaining network; otherwise stop. The final value of the sign at the moment of arriving at vertex B would indicate the most likely effect of the

The present invention encompasses the nucleic acid molecule of Figure 14C, comprising the sequence of EST AA481214 and proteins encoded by said nucleic acid molecule. The invention also relates to nucleic acid molecules capable of hybridizing to such a nucleic acid molecule under conditions of high stringency. By way of example and not limitation, procedures using such conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6x SSC, 50mM Tris-HCl (pH7.5), ImM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA and 500 mg/ml denatured salmon sperm DNA. Filters are hybridized for 48 hours at 65°C in prehybridization mixture containing 100 mg/ml denatured salmon sperm DNA and 5-20 x 106 CpM of ³²P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2x SSC, 0.01% PVP, 0.01% Ficoll and 0.01% BSA. This is followed by a wash in 0.1x SSC at 50°C for 45 minutes before autoradiography. Other conditions of high stringency which may be used are well known in the art.

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5.5.3. SIMULATION OF REGULATORY CASCADES

In an embodiment of the invention, an interactive graphical program is utilized for visualizing the scheme of regulatory relationships, "current" states of the substances, and active and inactive actions between pairs of substances. Such a program can be utilized for identification of genes which are associated with a specific disease. Currently, disease associated genes are discovered through positional cloning methods which combine methods of genetics and physical mapping with mutational analysis. The present invention provides a novel method for discovering disease associated genes. For simulating regulatory cascades, it is assumed that the time in a simulated regulatory system advances in discrete "quanta," or periods of time. The "state of substances" of the system for each discrete period of time is computed by: creating a set of substance objects, where a set of interactions between each created substance object is known, an initial state is specified. The time is initially set to zero. All defined actions are observed to confirm that the substances corresponding to the actions (i) exist, and (ii) are in the right initial states. Action is defined by a pair of substances that are in suitable states. The "subject" substance is in the inactive state,

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including for example yeast and/or nematode genes, that bear a significant similarity to the gene of interest or a specified domain of the corresponding protein are collected. Third, the identified genes are in turn subjected to a "domain analysis" to establish protein motifs which might suggest a function of these genes using, for example, HMMER software. Fourth, the selected genes are in turn used for database searches in EST databases (dbEST) and/or a non-redundant (nr) database to identify unknown genes that are potentially orthologous to the selected yeast and nematode genes. Once identified ESTs having different tumor suppressor domains may be linked using multiple PCR primers. Using routine cloning techniques, well known to those of skill in the art, a full length cDNA representing the gene of interest can be obtained.

Once new genes are identified by domain/motif analysis experimental searches may be carried out to isolate complete coding sequences and evaluate their tissue- and disease-specific expression patterns. In parallel their position with respect to regulatory networks can be identified as described below.

In a specific embodiment of the invention, an apoptosis related human gene was identified using the method described above. As a first step *C. elegans* genes containing either POZ or Kelch domains were identified. A Hidden Markov Model was developed using POZ and Kelch sequences from the *Drosophila* Kelch protein and any identified homologs. The resulting Hidden Marker Model was used to search through the collection of *C. elegans* protein sequences. One of the identified *C. elegans* genes contained a POZ domain, death domain, kinase domain and heat repeat. The presence of both a death domain and a kinase domain suggested that the protein functions as a regulatory protein.

A human EST database was searched using the protein sequence of the identified *C. elegans* gene and two sequences were identified (Figure 14A). A gene tree was computed to determine whether the identified human sequences were orthologs of the *C. elegans* gene. As depicted in Figure 14B, the human EST AA481214 appears to be a true ortholog of the *C. elegans* gene. Figure 14C presents the nucleotide sequence of the identified death domain gene. Figure 14D presents the amino acid sequence of the death domain protein.

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orthologous proteins with pairs of orthologous domains. After this correction, homologous networks are compared as described above.

Figure 10 is a diagram representing a hypothetical example of defining homologous protein networks in two different species using protein motifs, the diagram showing only two hypothetical proteins (lane 2) for species A and three hypothetical proteins (lanes 1, 3, and 4) for species B. Protein 1 in both species has motifs α and β , protein 2 has motifs δ , ϵ , and ζ , and proteins 3 and 4 have motifs δ and ζ , and ϵ , respectively. The motif analysis indicates that proteins 3 and 4 in species B may collectively perform the same function as protein 2 in species A.

5.5.2 GENE DISCOVERY BASED ON PROTEIN MOTIF/DOMAIN SEARCHES

The present invention provides yet another method for identifying genes that are homologous and perform the same or an analogous function in different species. The method of the invention comprises the following steps: (i) creating a database of sequences which comprise a motif or domain composition of a gene of interest using, for example, HMMER software; and (ii) searching additional databases for expressed sequence tags (ESTs) containing the domains and motifs characteristic for the gene of interest with HMMs of domains and motifs identified in step (i). In yet another embodiment of the invention, sequences may be searched which correspond to nucleotide sequences in an EST database or other cDNA databases using a program such as BLAST and retrieving the identified sequences. In an optional step, for each EST identified, sequence databases can be searched for overlapping sequences for the purpose of assembling longer overlapping stretches of DNA. Once identified, the ESTs can be used to isolate full length nucleotide sequences comprising the gene of interest using methods such as those described in Section 5.4, infra.

The general flowchart scheme for gene discovery analysis based on motif/domain search is shown in Figure 11. In a specific embodiment of the invention, the method referred to as the "phylogenetic reflection technique"comprises, first, defining the motif or domain composition of a gene of interest involved in a biological system of interest. Second, protein-coding genes from other species,

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In a specific embodiment of the invention a set of regulatory networks from different species, relating to the same biological system, apoptosis, for example, can be analyzed and visualized utilizing the following methods: (i) for each species functional information is collected relating to apoptosis; (ii) using the functional information, regulatory networks for each species comprised of interacting proteins and/or the genes involved in apoptosis are generated; (iii) the sequences of the interacting proteins and genes of each of the regulatory network are compared and for sequences showing similarity above a predetermined threshold range; and (iv) distinguishing between orthologs and paralogs using the methods set forth above.

An analysis similar to that performed using subtrees of sequences may be applied to classify protein functions as orthologous or paralogous actions. A "generalized" regulatory network maybe represented as a network wherein a substance as it occurs in a particular species is substituted with a cluster (i.e., subtree) of orthologous substances among species. In the final step of the analysis the clusters within each species are compared to one another, to identify missing genes.

Figure 11 depicts the regulatory relationships among hypothetical proteins (denoted with Arabic numerals) of hypothetical species A and B. As indicated in Figure 11A, an overlay of regulatory data for two species overlaps, but not completely. As indicated, protein 5 is known only for species B while protein 3 is known only for species A. The proteins in different species denoted with the same numeral are considered orthologous. As indicated, the regulatory relationships between a pair of proteins can be of three different kinds. Figure 9B, 9C, and 9D represent Boolean operations, OR, AND, and XOR, as arcs of the two regulatory relationships depicted in Figure 9A, the same operations being applicable to the set of vertices of the two regulatory relationships.

In some instances, orthologous networks in two distantly related taxa may have the same domains but arrangement of the domains between the related taxa may be different. In such a case, a one-to-one correspondence between orthologous proteins in closely related species has to be substituted with a one-to-many relationship among domains comprised within the proteins. For this purpose, a similarity object may be defined operating on pairs of motifs/domains in two proteins, and substitute pairs of

other species. The identified sequences are compared and for each pair of sequences showing similarity above a certain threshold, a similarity object is generated. A similarity object is generated if two sequences, nucleotide or amino acid, show significant similarity in database searches (p value < 0.001). The object retains the following information: (i) reference to similar substances *i.e.*, genes or proteins; (ii) significance of the similarity, similarity score and percent of identity; and (iii) coordinates of the similarity region within two compared sequences.

"Orthology objects" constitute a subset of "similarity objects" which satisfies one additional requirement, *i.e.*, that two similar sequences should be identified as orthologs by the tree-based algorithm described above. In identifying orthologs, if gene A is orthologous to gene B, and gene B is orthologous to gene C, gene A is necessarily orthologous to gene C.

In a specific embodiment of the invention, for each species under analysis, orthologous proteins or genes are identified. In a further embodiment of the invention, small orthologous molecules participating in a regulatory network for two or more species may also be identified. Where proteins, genes, or molecules are orthologs, the action of the protein, gene or molecule between species may be interchangeable. If more than two species are involved in the analysis, subtrees of orthologous substances and subtrees of orthologous actions are identified.

Once orthologous genes, proteins or molecules are identified in two or more species, by forming a reconciled tree, for example, a set of orthologous or paralogous regulatory networks can be analyzed and visualized using graph theory where arcs represent actions and vertices represent substances. Thus, the method of the invention may further comprise the following steps: (i) superimposing the orthologous regulatory networks from two or more species and searching for the actions (arcs) and substances (vertices) in the homologous networks that are represented in some taxa but absent in others; (ii) superimposing paralogous regulatory networks from the same taxa and searching for paralogous genes that are missing in some taxa; and (iii) computing a general regulatory network that summarizes common regulatory sequence relationships known for more than one species.

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multigene families through comparisons of regulatory networks for different species, searching expressed sequence tag (EST) databases, and simulation of regulatory cascades.

5.5.1. GENE DISCOVERY THROUGH ANALYSIS OF REGULATORY NETWORKS

The present invention provides a method for identifying undiscovered genes through comparisons of regulatory networks for different species where functionally similar regulatory systems are conserved. The amount of information available concerning regulatory genes and/or proteins in different organisms and their functional relationships allows one to reconstruct and compare regulatory networks. Since in most cases, the knowledge of all genes involved in almost any particular regulatory system is incomplete, a comparison of homologous networks within the same organism and between different species permits the identification of genes absent in a system under comparison.

The identified genes, being part of a regulatory network, are implicated as potentially contributing to a phenotype of a disease associated with the system under analysis. Using the methods of the present invention these putative disease genes can be cloned, mapped and analyzed for mutations directly, thereby omitting the expensive and time-consuming steps of positional cloning and sequencing of genomic regions. Gene discovery by analysis of regulatory networks is outlined in Figure 8. The analysis is initiated starting with a biological system (e.g., signaling pathway of genes involved in Bcl-2-regulated apoptosis in lymphocytes), a single gene (e.g., Bcl-2) or a gene family (e.g., caspases).

Initially, a specialized database is generated for comparison of regulatory networks between different species. For example, starting with a single candidate gene in a single species, a typical iteration in this process begins with identification of all known proteins and genes that are upstream and downstream with respect to it in regulatory hierarchies and the reconstruction of a network of interacting genes and proteins. Next, for each protein, a set of key domains and motifs is identified and this information is used to search for related proteins in humans and

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conducted to obtain overlapping sequences in dbEST. The search for overlapping sequences was performed using the program Iterate with EST Zs77e55.rl (gb/AA278224) as the search query. The search identified a single overlapping sequence. The search for overlapping sequences was performed using program Iterate with EST zs77e55.rl (gb/AA278224) serving as a query. The search returned a single overlapping sequence, namely HUMGS0012279 (dbj/C02407), thus showing that the two EST sequences found during the initial TBLASTIN search belong to the same gene. The complete sequence of the gene was assembled from the two ESTs using commercially available sequence assembly program SeqMan11(DNASTAR Inc., WI). The nucleotide sequence of the human Mad3 gene is presented in Figure 17B. The deduced amino acid sequence of which is presented in Figure 17C. The complete DNA sequence is also shown.

The present invention relates to nucleic acid molecules encoding the human Mad3 protein shown in Figure 17C. The invention also relates to nucleic acid 15 molecules that hybridize to the nucleic acid molecule of Figure 17B under conditions of high stringency and encode a Mad3 protein. By way of example and not limitation, procedures using such conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6x SSC, 50mM Tris-HCl (pH7.5), ImM EDTA, 0.02% PVP, 0.02% 20 Ficoll, 0.02% BSA and 500 mg/ml denatured salmon sperm DNA. Filters are hybridized for 48 hours at 65°C in prehybridization mixture containing 100 mg/ml denatured salmon sperm DNA and 5-20 x 106 CpM of ³²P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2x SSC, 0.01% PVP, 0.01% Ficoll and 0.01% BSA. This is followed by a wash in 0.1x SSC at 50°C for 45 minutes before autoradiography. Other conditions of high stringency which may be used are well known in the art.

5.5. <u>SIMULATION AND HYPOTHESIS TESTING</u>

The simulation and hypothesis testing methods of the invention, described in the subsections below, utilize specialized databases of gene/protein structures and interactions for identifying potentially undiscovered members of

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Then define similarity measure, σ , between S_{gi} and S_{sj} in the following way:

$$\sigma(S_{gi},S_{gj}) = 0 \text{ if } |S_{gi}| \neq |\{S_{gi}\}|, \text{ or } S_{sj}(S_{gi}) \neq S_{gi}, \text{ and}$$

$$\sigma(S_{gi},S_{gi}) = |S_{gi}|$$

The support of tree clusters by data can be measured using the bootstrap technique described in Felsenstein (1985, Evolution 39:783-791).

In an embodiment of the invention, the human antiquitin gene was identified using phylogenetic analysis. The aldehyde dehydrogenase gene family in humans can be subdivided into at least ten ancient subtrees characterized by different functions of corresponding proteins. These genes probably arose from a series of gene duplications of an ancestral gene which took place before the divergence of a common ancestor of Eukaryotes and Eubacteria.

The aldehyde dehydrogenase gene cluster is highlighted in Figure 6 which shows the original tree of ALDH sequences, the circled area indicating a sequence cluster where bacterial (*Bacillus subtilis*), plant (*Brassica napus*), and nematode (*Caenorhabditis elegans*) ortholog is present, but a human ortholog is not known. A random screening of cDNA libraries showed that a human ortholog, referred to as antiquitin, does exist. Figure 7 shows the same gene tree as in Figure 6 with an additional human protein referred to as antiquitin present in the tree.

In yet another embodiment of the invention, a human ortholog of the murine Max-interacting transcriptional repressor Mad3 was identified through phylogenetic analysis of a gene family. The gene tree was constructed as follows. The protein sequences of known members of the *Mad* gene family were extracted from GenBank database. The extracted sequences were aligned using multiple alignment program CLUSTALW running on Sun SPARC station. Redundant and non-homologous sequences as well as distant homologs from *S. cerevisiae*, *C. elegans*, *D. melanogaster* etc. were removed from the alignment. The refined set of sequences were realigned with CLUSTALW and a gene tree as presented in Figure 18A was computed. To identify a human ortholog of the Mad3 protein, a human dbEST at NCBI was searched with program TBLASTN using mouse Mad3 protein sequences as a query. Two highly homologous ESTs were identified and are presented in Figure 17A. To obtain a complete coding sequence a search was

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subtrees of orthologs in a gene tree, and then comparing the subtree in the gene tree with a species tree. A missing gene appears as a branch present in the species tree but absent in the gene tree. The algorithm for defining an orthologous gene subtree and predicting the undiscovered, or lost in evolution, genes is as follows:

Let T_g be the most likely gene tree identified with one of consistent tree-making methods from a set of properly aligned homologous genes $\{1, 2, ..., s\}$, such that one or more homologous genes from every species corresponds to pending vertices of T_g . Each gene is labeled with the species it comes from (1,...,s) adding subscripts to distinguish homologous genes from the same species whenever it is necessary. Let T_g be the true species tree (tree correctly reflecting speciation events which we assume to be known) for species $\{1, 2, ..., s\}$. Due to the biological meaning of T_s each species in this tree is represented only once. It is assumed that both T_s and T_g are binary, although it is straightforward to extend the algorithm described here to the case of multifurcated trees.

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- A1. For each pair of interior nodes from trees T_g and T_s , compute similarity $\sigma(S_{ei},S_{si})$.
- A2. Find the maximum $\sigma(S_{gi}, S_{gi})$.
- A3. Save S_{gi} as a new subtree of orthologs, save $\{S_{gi}\}$ $\{S_{sj}\}$ as a set of species that are likely to have gene of this kind (or lost it in evolution).
 - A4. Eliminate S_{gi} from T_g ; $T_g := T_g \setminus S_{gi}$.
 - A5. Continue A2 A4 until T_a is non-empty.

The following definitions apply:

Let S_{gi} be an *i*th subtree of T_g (corresponding to the *i*th interior node),

correspondingly, let S_{sj} be jth subtree of tree T_s .

Let $\{S_{gi}\}$ stand for an unordered set of species represented in S_{gi} such that each species is represented exactly once, and let $|\{S_{gi}\}|$ and $\{|S_{gi}|\}$ be the number of entries in $\{S_{gi}\}$ and the number of pending vertices in S_{gi} , respectively. Define by $S_{sj}(S_{gi})$ the unique subtree of S_{sj} that has leaves labeled exclusively with species from $|\{S_{gi}\}|$, so that each element of $|\{S_{gi}\}|$ is used i.e., that is, the unique subtree

obtained by eliminating from S_{sj} all species that are not present in $|\{S_{ej}\}|$.

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By applying phylogenetic analysis, *i.e.*, reconstruction of gene trees of gene/protein sequences, one can predict the existence of undiscovered genes in humans and other species in addition to identifying the function of a gene. Such a technique is a significantly more powerful tool for identification of new genes than mere sequence comparisons.

Methods of computing gene trees from a set of aligned sequences include the: (i) heuristic method based on an optimization principle which is not directly motivated by a probability model (Fitch, 1974 J. Mol. Evol. 3:263-268)), (ii) the maximum likelihood method (Goldman, 1990, Syst. Zool. 30:345-361; Yang et al., 1995, Syst. Biol. 44:384-399; Felsenstein, J., 1996, Methods Enzymol. 266-418-427); and (iii) the distance matrix tree making method (Saito, N. and Nei, M., 1987, Mol. Biol. Evol. 4:406-425). Since the data analyses of orthologs and paralogs often involve very distantly related sequences, the maximum likelihood method is preferably used for small data sets and the distance-matrix method in other instances.

To construct a reconciled tree according to the invention, the first step comprises a search for homologs in a publicly or privately available database such as, for example, GenBank, Incyte, binary BLAST databases, Swiss Prot and NCBI databases. Following the identification of homologous sequences a global alignment is performed using, for example, the CLUSTALW program. From the sequence alignment a gene tree is constructed using, for example, the computer program CLUSTLAW which utilizes the neighbor-joining method of Saito and Nei (1997, Mol. Biol. Evol. 4:406-425). Construction of a species tree is then retrieved from, for example, the following web site:

http://www.3.NCBI.NLM.NIH.GOV//taxomy.tax.html.

The species tree and gene tree are given as input into the algorithm described below, which integrates both trees into a reconciled tree. Agreement between the gene tree and the corresponding species tree for any given set of sequences indicates the identification of orthologs. In contrast, disagreement between the species and gene tree suggest a gene duplication that resulted in the formation of a paralog. Thus, through generation of a reconciled tree one can identify orthologs present in one species but missing in another. These can be deduced by forming

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amino acid or nucleotide replacements per site or in terms of millions of years (absolute geological time). In the former case, the average replacement rate in the majority of the published trees varies among tree branches, and the root-to-tip distances are different for different present day sequences. In the latter case, all root-to-tip distances are equal and the height of each interior node of the tree corresponds to the absolute geological time passed since the gene duplication corresponding to the interior node took place.

If a gene is unique, *i.e.*, represented with a single copy per genome rather than being a member of a family of similar genes, the correct gene tree depicting the origin of this gene in a few different species is identical to the species tree. In many instances, a single ancestral gene has been duplicated repeatedly during evolution to form a multigene family. A gene tree is constructed from a gene as it occurs in several species and reflects both speciation events and gene duplications within the same genome. Two homologous genes taken from different species that originated from the nearest common ancestor by speciation are referred to as orthologs, while any two genes that originated from the common ancestor via a series of events involving intragenomic duplications, or conversions, are called paralogs. The terms "ortholog" and "paralog" are applied to both nucleic acid and proteins herein.

If gene deletions are forbidden and all genes for all species represented in the tree are known, the gene tree can be reconfigured to recapitulate the species tree, such that each subtree contains only orthologous genes. This tree is referred to as a reconciled tree and is shown in Figure 5. Imperfect gene trees which contain incorrect or partial species subtrees can be used to build reconciled trees that indicate events of speciation, gene loss, and gene duplication.

Orthologs from different species in gene trees are usually clustered together, so that if all the existing homologous genes from different species were known, the same relationship of species would be recapitulated in each cluster of orthologous genes. Since in reality a considerable number of genes are not yet identified, the real gene trees contain incomplete clusters of orthologs that can be used for identification of the missing genes.

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lymphocyte apoptosis. This result indicates that the identified human Rpt1 homology may represent the gene in which genetic defects lead to CLL.

The amino acid sequence of the human Rpt1 gene is presented in Figure 15. The present invention relates to nucleic acid molecules encoding the human Rpt1 protein shown in Figure 15. The invention also relates to nucleic acid molecules capable of hybridizing to a nucleic acid molecule encoding the human Rpt1 protein presented in Figure 15 under conditions of high stringency. By way of example and not limitation, procedures using such conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6x SSC, 50 mM Tris-HCl (pH7.5), ImM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA and 500 mg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C in prehybridization mixture containing 100mg/ml denatured salmon sperm DNA and 5-20 x 106 CpM of ³²P-labeled probe. Washing of filters is done at 37°C for 1 h in a solution containing 2x SSC, 0.01% PVP, 0.01% Ficoll and 0.01% BSA. This is followed by a wash in 0.1 x SSC at 50°C for 45 minutes before autoradiography. Other conditions of high stringency which may be used are well known in the art.

5.4. GENE DISCOVERY THROUGH PHYLOGENETIC ANALYSIS OF GENE FAMILIES

The present invention provides a method for identifying novel genes comprising the following steps: (i) comparing a single sequence with a database; (ii) processing the output into a sequence alignment; (iii) computing gene trees; and (iv) analyzing the trees to predict the existence of undiscovered genes.

Figure 5 shows a "species tree," a "gene tree" and a "reconciled tree". A "species tree", as defined herein, is a graph depicting the correct order of speciation events leading to a set of present day species as defined by taxonomy. A "gene tree" is a graphical representation of the evolution of a gene from a single ancestral sequence in a common progenitor to a set of present-day sequences in different species. Where gene duplication has occurred, a branch is bifurcated. The branch lengths of a gene tree are most frequently measured either in terms of the number of

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Once developed, the specialized databases can be used to identify novel genes based on computation and analysis of phylogenetic trees for multigene families and analysis of homologous regulatory networks.

In a specific embodiment of the invention, a specialized database was generated using a set of keywords defining proteins involved in apoptosis (see, Figure 4). The specialized sequence database was referred to as Apoptosis 3. As a first step in generating the specialized database, a comprehensive set of articles describing the system of apoptosis or programed cell death was compiled. The articles were analyzed and information on regulatory pathways characterizing apoptosis from a variety of different organisms was extracted. Such pathways included those involved in MHC-T cell receptor interactions, inflammatory cytokine signal transduction, induction by light, γ-radiation, hyperosmolarity or heat shock, pathways involving immunoregulatory receptors or receptors having cytoplasmic domains, integrinrelated pathways and perforin/granzymeβ related pathways. The collected information was stored using Powerpoint (Microsoft) as a collection of graph/plots depicting the regulatory pathway. In addition, a list of proteins relevant to regulation of apoptosis was compiled.

Using the program Psi Retriever, sequences encoding the proteins relevant to regulation of apoptosis were retrieved from the non-redundant (NCBI) database of protein sequences and stored as a FASTA file. The FASTA file was then converted to a binary blast database using the program FORMATDB from the BLAST suit of programs. The BLAST suit of programs provides a set of programs for very fast comparisons of a single sequence to a large database. Both the database and the search or query sequence can be any combination of nucleotide and/or amino acid sequences.

In a working example described herein, the Apoptosis 3 database was used to compare genomic and cDNA sequences derived from the 13q region of human chromosome 13. This region of the chromosome is associated with Chronic Lymphocytic Leukemia (CLL). Using this method of analysis a human gene with significant homology to the mouse Rpt1 gene was identified. When the activity of Rpt1 is knocked out in mice, the regulatory effect is manifested as a block in T-

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interactions between them. Such databases are particularly useful for computation and analysis of regulatory networks between proteins. The semantic model is designed for representing substances, such as proteins and actions between them, and is based on widely accepted principles of object-oriented programming languages such as Java. Figure 3 is a diagram illustrating the object representation of molecules and relations between them. As indicated in Figure 3 there are six major classes, corresponding to the top-level classification of objects and actions: (i) a substance; (ii) a state of a substance; (iii) a similarity between substances; (iv) an action between substances; (v) a result of the action; and (vi) a mechanism that enables an action.

Figure 3 presents the class design graphically, listing the variables that represent the properties of each class or class object in the implementation. Classes can be made nested via the mechanism of "inheritance", *i.e.*, classes are defined starting with the most general ones and moving towards more specific classes.

Definition of more specific classes is simplified because the properties of the general classes are "inherited" by the specific classes and need not be redefined each time (see, Flanagan 1997, Java in a Nutshell, Second Edition. O'Reilley & Associates, Inc. Sebastopol, CA).

As shown in Figure 3, the two key object types in this scheme are substances (nodes of the graph representing regulatory networks) and actions (oriented edges connecting pairs of nodes), while result and mechanism objects are auxiliary to object action. Each substance object is characterized with a state. In this scheme, action is the most complicated object; each action object is characterized by a specific pair of substances participating in the action, one of which can be active and is referred to as Subject Substance and the second of which can serve as a substrate for the former and is referred to as Object Substance. Furthermore, for each action the initial and final states corresponding to interacting substances are defined. The property Time Required of each Action Object allows the setting of different durations for different actions (time is measured in relative units; see René Thomas and Richard D'Ari, 1990, "Biological Feedback," CRC Press Boca Raton, Ann Arbor, Boston).

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Hidden Markov Model method for building domain/motif models include neural network motif analysis (Wu, C.H. et al., 1996, Comput Appl Biosci 12, 109-18; Hirst, J.D., 1991, Protein Eng 4:615-23) and positional weight matrix analysis (Claverie, J.M., 1994, Comput Chem 18:287-94; Venezia, D., 1993, Comput Appl Biosci 9:65-9; Bucher, P. 1996, Comput Chem, 20:3-23; Tatusov, R.L., 1994, Proc Natl Acad Sci USA 91:12091-5).

Once a comprehensive collection of motifs/domains is created, each particular protein may be compared against a complete database of HMMs to identify known motifs and domains.

- 10 The Hidden Markov Model (HMM) is built using the following steps:
 - A1. Start with a motif/domain name and a single amino acid sequence representing a domain or motif.
 - A2. Do PSI-BLAST (BLASTPGP) search with the motif/domain sequence against a protein non-redundant database.
 - A3. Retrieve the sequences identified in the database search from the protein sequence database. Exclude low-complexity sequences, short or incomplete sequences and sequences with similarity score above a selected threshold of PPD value <0.001
 - A4. Align the set of sequences with CLUSTALW (or other multiple sequence alignment program).
 - A5. Use the set of aligned sequences for building HMM with the programs provided with HMMER and HMMER2 packages (see Hughey and Krogh 1996, J. Mol. Biol. 235:1501-1531).
 - A6. Do a new database search comparing new HMM with the nonredundant protein database.
 - A7. Continue steps A3-A6 until the convergence of the Markov model *i.e.*, until no new sequences are identified, or the maximum allowed number of iterations as defined by the user is reached. (Hugh R. and Krogh A., 1996, Comput. Appl. Biosci. 12: 95-107).
- In addition, in yet another embodiment of the invention, a specialized database may be designed to contain a semantic model of proteins and of the possible

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For example, but not by way of limitation, a specialized database may be prepared as follows. Protein and gene sequences may be provided, for example, by the Java program PsiRetrieve which allows for quick retrieval of protein or nucleotide sequences from binary BLAST databases by sequence accession number, keyword or groups of keywords, or species name. In addition, using the program PsiRetriever, sequences encoding the proteins of interest may be retrieved from the non-redundant (NCBI) database of protein sequences and stored as a FASTA file. The FASTA file is then converted into a binary blast database using the program FORMATDB from the BLAST suit of programs.

Known motifs/domains for proteins may also be collected using the flat file versions of major protein databases, such as SwissProt (http://expasy.hcage.ch/sprot) and the non-redundant database of NCBI (http://www3.ncbi.nlm.nih.gov). The databases can be downloaded and searched for the keywords "motif" and "domain" in the feature tables of proteins. In addition, existing databases of motifs and domains, such as BLOCKS (http://dupsas.Weizmann.ac.il/bcd/bcdparent//databanksblocks/hfml) and pfam(http://www.sanger.ac.uk//software/pfam; http://pfm.wustl.edu), can be downloaded (Henikoff et al., 1991, NAR 19:6565-6572). Still further, it is understood that any publically available database containing gene/protein sequences may be utilized to generate the specialized databases for use in the practice of the present invention.

Homologous sequences may be aligned using, for example, the CLUSTALW program (Higgins, et al. 1996 Methods in Enzymology 266: 383-402). A protein's sequence corresponding to each domain/motif can be identified, saved and used for building a Hidden Markov Model (HMM) of the domain/motif using a HMMER and HMMER2 packages (see, Durbin, R. et al. 1998 in Biological Sequence Analysis: Probablistic Models of Proteins and Nucleic Acids). HMMER and HMMER2 packages are useful for (i) building HMMs from sets of aligned protein or nucleotide sequences, and (ii) comparing the HMMs with sequence databases aimed at identifying significant similarities of HMMs with database sequences. Both nucleotide and protein databases can be used for this purpose. Alternatives to the

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Working with nucleotides implies that errors involving reading frames must be addressed. For example, working with a code of four letters, the nucleotide combination ATCTGTCACG could mean ATCT/GTCA or TCTG/TCAC or CTGT/CACG. Since the text is translated into a nucleotide combination, only one of these possibilities is correct. But BLAST can not distinguish between these solutions, *i.e.*, BLAST would potentially match a database sequence to a wrong reading frame in the query sequence, producing many nonsense results that could compromise the significance of true results.

The solution to this problem is a comma-free code. A comma free code knows only one correct reading frame. BLAST therefore does not produce any nonsense results. A comma-free code consists of only one permutation of a nucleotide combination. For example, given the nucleotide combination ATCC and its permutations CATC, CCAT and TCCA, only ONE of these permutations would be included in a comma-free code. The code in Appendix E does represent a comma free code. Comma-free codes were discussed in the early days of DNA research (Crick et al., Proc. Natl. Acad. Sci. 43:416-421).

In order to fine-tune the matching process, different BLAST parameters must be adjusted, for example: word size (which sets the size of the high scoring words, thus influencing the sensitivity of finding HSPs);mismatch penalty (exact vs approximate matching); numbers of alignments to show (true matches of low significance can sometimes be at the very end of the BLAST output, therefore many alignments have to be shown); and expectation value (which sets the significance value for matches in the output file).

5.3. GENERATION OF SPECIALIZED DATABASES

In accordance with the present invention, specialized databases may be developed that contain information derived from unpublished data, publications such as research articles, theses, posters, abstracts, etc. and/or databases concerning interactions among genes and proteins, their domain/motif structure, and their biological functions.

In addition, the script looks for plurals of words. For example, "interleukins" should be recognized as a protein name, although only the singular form, "interleukin", is in the database.

The final result consists of the original journal article with XML tags surrounding the gene and protein names. This is done using the same script as in Appendix G:

blocked <phr sem="gp">T cell antigen receptor</phr> (TCR)- and <phr sem="gp">CD28</phr>-mediated <phr sem="gp">IL-2</phr> gene transcription. Therefore, <phr sem="gp">Rap1</phr> functions as a negative regulator of...

To adapt the problem to BLAST's statistical foundation, different measures were undertaken to limit the output to the most relevant gene and protein names.

BLAST is sensitive to the search space the program works in. Thus, given a long query sequence and a large sequence database, matches have a lower statistical significance because the chances are higher that the matches could have occurred by chance alone. In addition, matches with few letters have a lower statistical significance than matches with many letters. In order to find all true matches with any significance level, some measures were undertaken to address this problem. For example, (i) the query sequence was divided into 10 equal length parts, i.e., the journal article was divided into 10 parts and 10 different queries are run on each part separately; (ii) the sequence database (with the gene and protein names) is separated into 5 databases, each containing protein/gene names of different length; (iii) gene and protein names with less than 3 letters in the database were 'expanded', i.e., spaces were added at the beginning and the end of the name. Doing so, the statistical significance of a match containing a short name was higher. A space does not only include an empty character. For example, a gene name "k4" could occur in a journal article as "kinin 4 (k4)". It was therefore important to define several characters as substitutes for a space character. The alphabet in Appendix E defines the nucleotide combination ATCC as such a substitute.

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using a Perl-script (see Appendix F). The script shown in Appendix G scans the output file, which is sometimes several megabytes long, for any segments that start at position 1 of the database sequence (thus disregarding any segments that are only part of the sequence). In addition, the script allows for 10% mismatches between the aligned sequences for long sequences (as shown in the script of Appendix E), or 0% mismatches for short sequences. After scanning the output file, an intermediary file that lists the candidate sequences is created:

tran|365|381|gp|18493 tran|1|17|gp|18493 10 peci|549|565|gp|58106 il-2|621|637|gp|82396 il-2|325|341|gp|82396 gati|193|209|gp|92088 prod|641|657|gp|52292 15 rap1|105|121|gp|49898 spec|545|561|gp|33183 crip[385[401|gp[118905 crip|21|37|gp|118905 as|161|177|gp|133961 20 her|65|77|gp|88411

The intermediary file lists the name of the sequence, followed by the starting and end point in the query sequence (corresponds to where the two sequences matched), the semantic class of the name (protein, gene or protein/gene). The last number is not considered.

The intermediary file is then scanned by another Perl program (Appendix G). This program compares the starting end points with the actual text, making sure that the matched name is an 'autonomous' entity in the query text. For example, while "per" in " per gene" should be recognized as a gene name, "per" in "personal" should not be recognized as a gene name. The program recognizes other characters than the space character delimiting an 'autonomous' gene or protein name.

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the absence of costimulation, T cells activated through their antigen ..." is translated into

A query is then used to match the translated journals against the nucleotide representation of gene and protein names in the BLAST database. The query is executed using the blastall program that is included in the BLAST package. The query line looks like:

blastall -p blastn -d FASTA.dat -i query.txt

The flag 'p' denotes the sub-program (blastn is a sub-program of blastall that performs nucleotide matches), 'd' denotes the file that contains the FASTA entries and 'i' denotes the translated query text.

Significant alignments associated with gene and protein names are listed in the BLAST output file. This is an excerpt from a BLAST output file:

gi|63624 species,gp,ner

20 Length = 12

Score = 24.4 bits (12), Expect = 3e-05

Identities = 12/12 (100%)

Strand = Plus / Plus

Query: 729 acagaacgacct 740

25 Sbjct: 1 acagaacgacct 12

The first line denotes the database entry. The second line denotes the database sequence length, followed by the alignment score and the E-value. The next line indicates paired matches, mismatches and gapped alignment (the latter two are not shown in this example). The lines 'Query' and 'Sbjct' show the actual alignment between the query and database sequence. This output file is subsequently processed

hox al wac 3'-end pit-1/ghf-1 variant [...]

This list of gene and protein names is translated into a different alphabet system by substituting each character in the name with a predetermined unique nucleotide combination. The conversion chart is listed in Appendix E. The encoded names are then imported into the BLAST database using the FASTA format. For example, the first entry in the list above is "gfap gamma." After translation using the conversion chart, the same name appears as follows:

AGCAACTAAACACCCATCCAAGCAAACACACACACAAAC
Thus, the complete FASTA entry looks like this:
>gi|1 species,gp,gfap gamma

AAGCAACTAAACACCCATCCAAGCAAACACACACACAAAC

In FASTA, the definition line (marked with '>') contains information about the database entry. This line can contain any kind of information. The information important for this particular example is the third entry in the definition line, 'gp', that specifies that the name can represent a gene or a protein. If the name is unambigous, then the definition line states that the name is only associated with a gene ('g') or protein ('p'). The fourth entry in the definition line is the name of the protein or gene, "gfap gamma" in this case.

The second line in the FASTA format normally contains the actual sequence of the protein/gene. In the example presented, the second line contains the translated protein or gene name.

All gene and protein names are translated into the nucleotide representation and converted into the FASTA format. Then, the database containing these FASTA entries are specially compiled for use in BLAST queries using a program that is included in the BLAST package called "formatdb".

Thus, the scientific journals are translated, using the same nucleotide combinations, into a continuous string of nucleotides. For example, the sentence "In

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signifying that the agent has not been specified; the second argument is a protein with the value jnk. The second argument is the target:

[action,inactive,[protein,bad],[action,phosphorylate,x,[protein,jnk]
In summary, a computer system has been disclosed that generates
structured information concerning protein and gene interactions and relationships.

5.2. USE OF BLAST FOR FINDING GENE AND PROTEIN NAMES IN JOURNAL ARTICLES

In a specific embodiment of the invention, an exhaustive list of gene and protein names, extracted from GeneBank, is translated into a different alphabet system by substituting each character in the name with a predetermined unique nucleotide combination. The encoded names are then imported into the BLAST database using the FASTA format. The scientific journals are translated, using the same nucleotide combinations, into a continuous string of nucleotides. A query is then used to match the translated journals against the nucleotide representation of gene and protein names in the BLAST database. Significant alignments associated with gene and protein names are listed in the BLAST output file, which is subsequently processed using Perl-scripts. The final result consists of the original journal article with XML tags surrounding the gene and protein names.

To adapt the problem to BLAST's statistical foundation, different measures were undertaken to limit the output to the most relevant gene and protein names. In addition, in order to fine-tune the matching process, different BLAST parameters were adjusted, such as the word size (which sets the size of the high scoring words, thus influencing the sensitivity of finding HSPs) and mismatch penalty (exact vs approximate matching).

In a specific embodiment of the invention, gene and protein names are extracted from GeneBank's gene symbol index file. The following is an excerpt of the file after discarding entries that are either composed of only numbers or of less than two alphabetic letters:

gfap gamma

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repeated until an analysis of each segment is obtained or until segmenting is no longer possible.

Mode 3 requires a well-formed pattern for the "largest" prefix of the segment, *i.e.*, usually at the beginning of the segment. This occurs when a sentence contains a pattern at the end which is not in the grammar but a beginning portion that is included. For example, in "bad inactivates jnk at this time", the beginning of the sentence "bad inactivates jnk" will be parsed and the remainder will be skipped.

Mode 4 requires that undefined words be skipped and an analysis be attempted in accordance with Mode 1. Mode 4 is useful where there are typographical errors and unknown words. For example, in the phrase "abc bad inactivates jnk", the word *abc* is unknown to the system and will be ignored but the remainder of the phrase will be parsed.

Mode 5 first requires that the first word or phrase in the segment associated with an action be found. Next, an attempt is made to recognize the phrase starting with the leftmost recognizable argument. For example, in "during bad inactivates jnk on the fifth day," the phrase "bad inactivates jnk" will be parsed and the remaining words will not be. If no analysis is found, recognition is retried at the next possible argument to the right. This process continues until an analysis is found.

Process_sects with get_section and parse_sentences gets each section and generates intermediate output for the sentences in each section.

Write produces the output as a list consisting of relations and interactions

Setargs sets arguments or parameter values based on user input or by default.

The structured output generated by the GENIE program uses a frame-based representation. Each frame specifies the informational type, the value, and arguments or modifier slots which are also frames. Consider the text data input "bad inactivates the phosphorylation of jnk." A corresponding output, as shown below, is a frame denoting an action, which has the value inactivate; in addition, there are two arguments. The first argument is a protein bad and the second argument is an action with the value phosphorylate, which has two arguments. The first argument is x

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mode) and Protocol (html or plain). *Process_sents* is called by another predicate, after user-specified parameters have been processed.

The parsing modes are selected by GENIE so as to parse a sentence or phrase structure using a grammar that includes one or more patterns of semantic and syntactic categories that are well-formed. For example, for the phrase "bad inactivates ink", a legitimate pattern can be substance1 action substance2, wherein substance1 = protein bad, action = "inactivates" and substance2 = "jnk." However, if parsing fails, various error recovery modes are utilized in order to achieve robustness. The error recovery techniques use methods such as segmenting the sentence, processing large chunks of the sentence, and processing local phrases. Each recovery technique is likely to increase sensitivity but decrease specificity and precision. Sensitivity is the performance measure equal to the true positive rate of the natural language processing, i.e., the ratio of information extracted by the natural language processing system that should have been extracted. Specificity is the performance measure equal to the true negative information rate of the system, i.e., the ratio of information not extracted by the NLP system that should not have been extracted. Precision is the reliability of the system, i.e., the ratio of information extracted correctly compared to all the information that was extracted. In processing a report, the most specific mode is attempted first, and successive less specific modes are used only if needed.

In accordance with the preferred embodiments of the present invention, the parser of Figure 2 includes five parsing modes, Modes 1 through 5, for parsing sentences or phrases. Nominally, the parser is configured to first select Mode 1. If Mode 1 is not possible, the program continues with Mode 2 and so forth until parsing is complete. With Mode 1, the initial segment is the entire sentence and all words in the segment must be defined. This mode requires a well-formed pattern for the complete segment.

Mode 2 requires that the sentence or phrase be segmented at certain types of words or phrases, *e.g.*, " is attributable to." Here, an attempt is made to recognize each segment independently, *i.e.*, a first segment ending with the word "is" and a second segment beginning with the word after "to." The segmenting process is

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formed syntactic and semantic patterns in the sentence and to generate structured output forms. The parser proceeds by starting at the beginning of the sentence element list and following the grammar rules. When a semantic or syntactic category is reached in the grammar, the lexical item corresponding to the next available unmatched element is obtained and its corresponding lexical definition is checked to see whether or not it matches the grammar category. If it does match, the word or phrase is removed from the unmatched sentence list, and the parsing proceeds. If a match is not obtained, an alternative grammar rule is tried. If no analysis can be obtained, an error recovery procedure is followed so that a partial analysis is attempted. The actual grammar used for GENIE appears as Appendix D.

The parser module of GENIE uses the lexicon, and a grammar module to generate target forms. Thus, in addition to parsing of complete phrases, subphrase parsing can be used to an advantage where highest accuracy is not required. In case a phrase cannot be parsed in its entirety, one or several attempts can be made to parse a portion of the phrase for obtaining useful information in spite of a possible loss of information.

Conveniently, each module is software-implemented and stored in random-access memory of a suitable computer, e.g., a work-station computer. The software can be in the form of executable object code, obtained, e.g., by compiling from source code. Source code interpretation is not precluded. Source code can be in the form of sequence-controlled instructions as in Fortran, Pascal or "C", for example. Alternatively, a rule-based system can be used such a Prolog, where suitable sequencing is chosen by the system at run-time.

An illustrative portion of the GENIE system is shown in the Appendix D in the form of a Prolog source listing with comments. The following is further to the comments.

Process_sents with get_inputsents, process_sects and outputresults reads in an input stream, processes sections of the input stream according to parameter settings, and produces output according to the settings, respectively. Among parameters supplied to Process_sents are the following: Mode (specifying the parsing

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syntactic and semantic. The syntactic lexicon for actions specifies the main syntactic category such as "v" for verb, "ving" for progressive form of verb, and "activation" for noun. The semantic entries for actions not only categorize the actions, but also specify features for each action. For example, one feature provides the number of arguments that are expected for the action, *i.e.*, some actions are associated with two arguments because they have an agent and a target as "inactivate", and others just have an agent "mutate." The lexicon of substances and structures appears as Appendix A; the syntactic lexicon for actions appears as Appendix B; and the semantic lexicon of actions appears as Appendix C.

A second feature specifies whether or not the arguments should be reversed when obtaining the target form. For example the arguments of "attributable to" should be reversed, *i.e.*, in "the phosphorylation of jnk is attributable to the activation of bad", the underlying action is "cause" (from "attributable to"), the agent is the "activation of bad" and the target is "the phoshorylation of jnk"), whereas the arguments of "activates" is not(i.e. in "jnk activates bad", the agent is "jnk" and the target is "bad").

Figure 2 shows a preprocessor module of GENIE by which natural-language input text is received. The preprocessor thus performs lexical lookup to identify and categorize multi-word and single word phases within each sentence. The output of this component consists of a list of word elements where each element is associated with a word or multi-word phrase in the report. For example, assuming that the sentence "bad functions as a negative regulator of the activation of jnk" is at the beginning of the report, it would be represented as a list of elements where each element is a word or phrase. For example, element 1 is associated with "bad", element 2 with the multi-word phrase "functions as a negative regulator of", element 8 with "the", and element 9 with "activation". The remainder of the list of word positions would be associated with the remaining words in the report. Some of the phrases may not need lexical lookup because they already have been tagged by a previous component. Such a tagging system is described below in Section 5.2.

The second component of the GENIE system is the parser. It utilizes the grammar and categories assigned to the phrases of a sentence to recognize well-

A natural-language phrase included in text document is understood as a delimited string comprising natural-language terms or words. The string is computer readable as obtained, e.g., from a pre-existing database, a keyboard input, optical scanning of typed or handwritten text, or processed voice input. The delimiter may be a period, a semicolon, an end-of-message signal, a new-paragraph signal, or any other suitable symbol recognizable for this purpose. Within the phrase, the terms may be separated by another type of delimiter such as a blank or another suitable symbol.

As a result of phrase parsing, terms in a natural-language phrase are classified, (e.g., as referring to a gene, a protein, or their interactions) and the relationships between the interactions are established and represented in a standard form. For example, in the sentence "Rap inhibited fyn", the structured form would be:

[action,inactivate,[protein,rap],[protein,fyn]].

In such an example, the interaction is "inactivate", the agent is "Rap" and the target is "fyn." More complex sentences consisting of nested relationships, such as "The activation of BAD was suppressed by the phosphorylation of JNK" can also be parsed and represented appropriately. The structured output form for this sentence would be: [action,inactivate,[action,phosphorylate,x,[protein,jnk],[action,activate,x,[protein,bad]]

In the first example, the primary interaction is "inactivate"; in the second example, an interaction "phosphorylate" is the agent where the protein "jnk" is its target (the agent of "phosyphorylate" in not specified and thus is represented as "x"). In this example, the target of "inactivate" is also an interaction "activate" where the target is the protein "bad" and the agent is unknown.

While parsing is based on both syntactic and semantic grammatical patterns, the substances in a domain are normally only semantic categories such as "protein", "gene", and "small molecule." There are no corresponding syntactic categories needed for these substances because they are normally all nouns. However, each action can be categorized both semantically and syntactically. An action, which is a semantic category, can generally occur syntactically as a verb "inactivate" or as a noun "inactivation." Therefore there are two sets of lexical entries for the actions:

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5.1. THE NATURAL LANGUAGE PROCESSING

The present invention relates to a natural language processing system that is designed to parse the electronic versions of articles published in journals that report on structural interactions among genes and proteins. The system provides a method for extracting information on interactions among genes and proteins, their domain/motif structure, and/or their sub-cellular and tissue expression/distribution patterns, followed by computer representation of such information.

The general natural language-processing system of the invention is schematically depicted in Figure 2. The collection phase automatically collects articles from appropriate literature, and selects articles that contain relevant information using Keyword search techniques. In the next phase, the preprocessor standardizes the selected articles so that they consist of tagged ASCII text where the tags delineate critical components of the article. The next phase, termed the extraction phase, retrieves and classifies biological entities, *i.e.*, as names of proteins, genes and small molecules. In addition, the relationship extraction phase recovers structural relationships between the entities. This phase is followed by a phase which performs an analysis of the sequence of events.

The final phase of the system processes the output extracted from an article to remove redundancies, inconsistencies and to incorporate implicit information before adding the extracted knowledge consisting of biological entities, their attributes, conditional constraints, and relationships between them, for subsequent use in analysis and hypothesis testing. The information extraction system as depicted in Figure 2, referred to herein as "GENIE," is designed for use as a general processor within the domain of genomics literature although the system may also be used in other specialized domains. GENIE is an adaptation of MedLEE developed for the medical domain. GENIE uses the same source code as MedLEE but the Lexicons and grammar were adapted for genomics literature.

The information extraction system of the present invention is described below, by way of example, with reference to the genomics domain uses of GENIE. It is written in Quintus Prolog and uses the Unix or Windows operating systems, as described in detail below.

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Figure 17B. Nucleotide sequence of the human Mad3 gene.

Figure 17C. Complete sequence of the human Mad3 protein. A search was conducted to identify overlapping sequences. The complete sequence of the gene was assembled and the amino acid sequence deduced. The translated human Mad3 sequence consists of 206 amino acid residues 81% of which are identical to the mouse Mad3 protein.

Figure 17D. Multiple alignment of the human Mad3 amino acid sequence with known Mad proteins.

Figure 18A. Phylogenetic tree indicating relationship between three known mouse Mad genes and their two human homologs.

Figure 18B. Phylogenetic tree including new human Mad3 sequence.

The phylogenetic tree indicates that the new human gene belongs to the family of Mad proteins and is an ortholog of mouse Mad3.

5. DETAILED DESCRIPTION OF THE INVENTION

The present invention provides methods for identification of novel genes comprising: (i) generating specialized databases containing information on gene/protein structure, function and regulatory interactions and, (ii) sequence analysis which includes homology searches and motif analysis thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest.

The specialized databases are constructed utilizing information concerning gene/protein structure or function derived from unpublished data, research articles and/or existing databases. The specialized databases can be used to identify novel genes by: (i) searching for motif/domain combinations characteristic for a putative gene of interest; (ii) phylogenetic tree analysis of homologous genes for predicting the existence of yet undiscovered genes; (iii) comparing members of interactive gene/protein networks from different species for predicting the existence of yet undiscovered genes; and (iv) testing a hypothesis with regard to known interactions of homologs from other species in regulatory pathways.

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Figure 11A and 11B are diagrams respectively representing hypothetical examples of evaluating the impact of a "knockout" of hypothetical gene A on the expression of a hypothetical gene B. The effect of knock-out of gene A calculated by multiplication along the shortest pathway connecting genes A and B is inhibition of gene B, the resulting effect being zero if the orientation of only one arc in the same pathway is reversed;

Figure 12 is a flow chart representing the scheme of gene discovery analysis involving motif/domain analysis in accordance with the present invention; and

Figure 13 Identification of genes in *C. elegans* containing either POZ or kelch domains. The protein excession numbers are indicated adjacent to the different protein domains. The protein corresponding to accession number gi/1132541 contains a POZ domain, death domain, kinase domain and heat repeat.

Figure 14A. Two human sequences with the closest homology to the *C. elegans* sequence gi/1132541.

Figure 14B. Computed gene tree indicating that the identified human gene represents an ortholog of the *C. elegans* gene gi/1132541.

Figure 14C. Nucleotide sequence of the death domain gene.

Figure 14D. Deduced amino acid sequence of the death domain

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Figure 15. Identification of candidate gene implicated in the etiology of Chronic Lymphocytic Leukemia (CLL). Sequence homology between a CLL region open reading frame and mouse Rpt1 (sp/P15533/RPT1) is presented.

Figure 16A-B. Model of regulatory functions of Rpt1. Figure 16A indicates that in mouse T lymphocytes Rpt1 serves as a repressor of the gene for interleukin 2 receptor (IL-2R). Figure 16B demonstrates that when Rpt1 is knocked out, the regulatory effect is manifested as a block of the apoptotic pathway for T-lymphocytes resulting in accumulation of T-lymphocytes in blood.

Figure 17A. Two EST sequences identified by searching a protein dbEST using the mouse Mad3 protein as a query.

is a graph depicting a history of a few genes from the same species, where each species can be represented by multiple paralogous genes (because the set of known genes is incomplete for most genomes, and there are often multiple representations of the same gene family in the same genome, the gene tree can be drastically different from the corresponding species tree); and a "reconciled tree", which is the gene tree that would be obtained if gene deletions were completely forbidden and all genes were known for all species under analysis;

Figure 6 shows the original tree of ALDH sequences, indicating sequence clusters where bacterial, plant, fungal and nematode orthologous genes are present, but a human ortholog was not yet known;

Figure 7 shows the same phylogenetic tree as in Figure 6 with an additional human protein, referred to as antiquitin which was discovered by the method of the invention;

Figure 8 is a schematic diagram illustrating functional network-based gene discovery in accordance with the present invention;

Figure 9A presents diagrams depicting the regulatory relationships among hypothetical proteins (denoted with Arabic numerals) of hypothetical species A and B. Proteins in different species denoted with the same numeral are considered orthologous. The diagrams show that regulatory relationships between a pair of proteins can be of three different kinds;

Figure 9B, 9C, and 9D are diagrams representing Boolean operations OR, AND, and XOR, on arcs of the two oriented graphs of Figure 9A, the same operations being applicable to the set of vertices of the two oriented graphs;

Figure 10 is a diagram representing a hypothetical example of defining homologous protein networks in two different species using protein motifs, the diagram showing only two hypothetical proteins (1 and 2) for species A and three hypothetical proteins (1, 3, and 4) for species B. Protein 1 in both species has motifs α and β, protein 2 has motifs δ, ε, and ζ, and proteins 3 and 4 have motifs δ and ζ, and ε, respectively. The motif analysis can indicate that proteins 3 and 4 in species B may collectively perform the same function as protein 2 in species A;

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predict undiscovered genes. This program also includes a set of tools for generating motif/domain models from multiple sequence alignments of known genes and for using these models for extraction of structurally and/or functionally homologous sequences from databases which contain raw sequence data.

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The invention further provides for a simulation and hypothesis testing program which relies on the specialized databases of gene/protein interactions for identifying potentially undiscovered members of multigene families through comparisons of regulatory networks for different species and testing hypotheses with regard to regulatory cascades. A comparison of homologous regulatory networks within the same organism and between different species of organisms will allow the identification of genes absent in one of the systems under comparison, thus providing a set of candidate genes. In this way, genes that contribute to the phenotype of a specific disease associated with a particular biological system under analysis may be identified, mapped and subjected to mutational analysis and functional studies.

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4. BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a block diagram illustrating the three major programs of the method according to the present invention: (i) the generation of specialized databases based on information on gene/protein structure, function and regulatory interactions derived from research papers and databases; (ii) sequence analysis; and

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Figure 2 is a block diagram of an information extraction system in accordance with a preferred embodiment of the present invention;

(iii) simulation and hypothesis testing;

Figure 3 is a diagram illustrating the object representation of molecules and relations between them;

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Figure 4 shows a set of keywords defining proteins involved in apoptosis pathways, these keywords having been utilized for generating a specialized sequence database Apoptosis3, this list having been compiled manually for testing the concept of specialized databases;

Figure 5 shows a "species tree," which is a graph depicting the correct order of speciation events leading to a set of present day species; a "gene tree," which

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3. SUMMARY OF THE INVENTION

In accordance with the present invention there is provided methods for identification of novel genes comprising (i) generating one or more specialized databases containing information on gene/protein structure, function and/or regulatory interactions; and (ii) searching the specialized databases for homology or for a particular motif and thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest.

The invention is based, in part, on the observation that functionally similar regulatory systems are generated during evolution by genetic duplication of ancestral genes. Thus, by comparing phylogenetic trees or regulatory networks and identifying genes and/or proteins absent in one system under comparison, the existence of as yet unidentified genes and/or proteins can be predicted. To make meaningful comparisons of phylogenetic trees it is necessary to distinguish between orthologs and paralogs. The present invention provides a method useful for discriminating between orthologs and paralogs and inferring the existence of as yet unidentified genes and/or proteins.

The present invention relates to natural language processing and extraction of relational information associated with genes and proteins that are found in genomics journal articles. Specifically, the natural language processing system of the invention is used to parse the articles published in biological journals focusing on structure and interactions among genes and proteins followed by computer representation of such interactions.

In accordance with the present invention, specialized databases are developed that contain information on gene/protein structure and interactions based on information derived from preexisting databases and/or research articles including information on interactions among genes and proteins, their domain/motif structure and their subcellular and tissue expression/distribution patterns.

The invention relates to a sequence analysis program which utilizes the specialized database for comparison of a single sequence, processing the output into a sequence alignment, computing phylogenetic trees, and analyzing these trees to

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Two homologous genes taken from different species that originate from the nearest common ancestor by speciation are referred to as orthologs, while any two genes that originate from a common ancestor via a series of events involving intragenomic duplications are call paralogs. Tatusov et al. (1994, Proc. Nat.l, Acad. Sci USA 91:12091-12095) describe comparisons of proteins encoded by the genomes of different phylogenetic lineages and elucidation of consistent patterns of sequence similarities permitting the delineation of clusters of orthologous groups (COGs). Each COG consists of individual orthologous genes or orthologous groups of paralogs from different phylogenetic lineages. Since orthologs typically have the same function, the classification of known genes and proteins into clusters of orthologous groups permits the assignment of a function to a newly discovered gene or protein by merely classifying it into a COG. Although Tatusov describes a method for assigning a function to a newly discovered gene, he does not describe a method for predicting the existence of undiscovered genes. In addition, Yuan, et al. attempted simultaneous reconstruction of a species tree and identification of paralogous groups of sequences and detection of orthologs in sequence databases (Yuan et al., 1998, Bioinformatics 143:285-289).

Other groups have aimed at capturing interactions among molecules through the use of programs designed to compare structures and functions of proteins 20 (Kazic 1994, In: Molecular Modeling: From Virtual Tools to Real Problems, Kumosinski, T. and Liebman, M.N. (Eds.), American Chemical Society, Washington, D.C. pp. 486-494; Kazic, 1994, In: New Data Challenges in Our Information Age Glaesar, P.S. and Millward, M.T.L. (Eds.). Proceedings of the Thirteenth International CODATA Secretariat, Paris pp. C133-C140; Goto et al., 1997, Pac. 25 Symp. Biocomput. p. 175-186; Bono et al., 1998, Genome Res. 8:203-210; Selkov et al., 1996, Nucleic Acids Res. 24:26-28). These projects are significantly different from the inventive methods described herein because they do not describe methods for deducing the existence of as yet unknown genes based on comparisons of regulatory pathways and gene structure between one or more species. The present invention 30 provides a method for increasing the sensitivity of analysis methods through the generation of specialized databases.

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loci, can hardly be found using this strategy because of the complications associated with multiple loci linkage analysis.

Specialized databases for homology searches have also been utilized in disease gene discovery projects. In recent years a number of efficient sequence comparison tools have been developed such as the BLAST (Basic Local Alignment Search Tool) family of programs designed for comparison of a single "search sequence" with a database (see Altschul et al., 1990, J. Mol. Biol. 215:403-410; Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402), the family of Hidden Markov Model methods for comparison of a set of aligned sequences that usually represent a protein motif or domain with a database (e.g., Krogh et al., 1994, J. Mol. Biol. 235:1501-1531; Grundy et al., 1997, Biochem Biophys. Res. Commun. 231:760-6) and various other comparison tools (Wu et al., 1996, Comput. Appl. Biosci 12:109-118; Neuwald et al., 1995, Protein Sci. 4:1618-1632; Neuwald, 1997, Nucleic Acids Res. 25:1665-1677).

When used in disease gene discovery projects, homology searches can be enhanced by creating specialized databases that utilize statistical analysis for evaluating significance of sequence similarities in comparison of new sequences with a database of known sequence. Such databases are fine-tuned to the size of the database used (Altschul et al., 1990, J. Mol. Biol. 215:403-410; Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402), so that the same level of homology between a search sequence and a database sequence can be determined to be highly significant if the search sequence is compared with a smaller database, or insignificant and thus undetectable, if the search sequence is compared with a larger database.

In alternatives to standard homology searches, in projects oriented towards gene discovery, researchers usually have some *a priori* knowledge about the set of genes/proteins that might display important similarity to the unknown new gene. Therefore, selecting an *a priori* defined set of genes/proteins for comparison with new experimental sequences is a feasible and useful strategy. This strategy was successfully applied to search for homologs of disease genes in yeast and nematode genomes by Mushegian et al. (1997, Proc. Natl. Acad. Sci USA 94:5831-5836).

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2.2. IDENTIFICATION OF NOVEL GENES

A variety of different methods are currently utilized for the identification and characterization of novel genes. Perhaps the most widely used method for generating large quantities of sequence information is via high throughput nucleotide sequencing of random DNA fragments. A disadvantage associated with this gene discovery technique is that in most instances when genes are identified their function is unknown.

For identification of specific disease genes, positional cloning is currently the most widely used method. The positional cloning approach combines methods of formal genetics, physical mapping and mutation analysis and usually starts with a precise description of the disease phenotype and a tracing of the disease through families of affected individuals. Genetic linkage data obtained from the analysis of affected families frequently allows the determination of an approximate genomic localization of the candidate disease gene with a precision of several millions of nucleotides. Once localized, the genetically defined chromosomal region is then recovered from genomic libraries as a contiguous set of genomic fragments. Genes residing in the disease-related region are determined by analysis of transcripts that are transcribed from the genomic fragment. From this analysis an initial set of candidate genes for a particular disease are identified based on the presence of the gene product in the biological system affected by disease and a correlation between its expression pattern and the pattern of disease progression.

Important information for selection of candidate genes also comes from analysis of their homology with genes known to be part of the same or related biological system. Finally, the ultimate proof of association between a gene and a genetic disorder comes from mutational analysis of a gene in patients affected by the disorder and from demonstration of a statistical correlation between occurrence of mutation and the disease phenotype.

Although positional cloning is a powerful method for gene discovery, the experimental method is extremely tedious and expensive. Moreover, disease genes implicated in genetically complex disorders, *i.e.*, those controlled by multiple

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Natural language processing is an automated system that provides for a complex of programs for automatic retrieval of information from text analysis and for the computer representation of that information in a form that allows efficient access and extraction of that information. MedLee (Medical Language Extraction and Encoding System) has recently been successfully used for processing different types of medical texts as described in co-pending United States Patent Application Serial Number 09/370,329, incorporated herein in its entirety by reference (see also, Friedman et al., 1994, J. Amer. Med. Inf. Assoc. 1:161-174; Hripcsak et al. 1995, Ann. Intern. Med. 122:681-688; Hripcsak et al., 1998, Meth. Inform. Med.; Jain et al., 1996, Proc. AMIA Annu. Fall Symp. 542-546; Knirsch et al., 1998). When tested, MedLEE was on average as successful in retrieving reports associated with specified clinical connections as twelve medical experts invited for evaluation of the system.

Another text analysis technique has recently been developed that combines finite-state machines with statistical machine learning approaches. These models extract detailed semantic information from texts (e.g., see Hatzivassiloglou 1996, In Klavens, J.L., and Resnick, P.S. (eds) *The Balancing Act: Combining Symbolic and Statistical Approaches to Language*, MIT Press, Cambridge, MA) when extensive prior knowledge about the domain is not available. The techniques have been subsequently applied to the tasks of (i) automatically identifying medical terms for the automated summarization of research articles reporting on clinical studies and (ii) sanitizing sensitive information in patient records so that they can be widely disseminated for research purposes.

A number of projects have also been developed as statistical information extraction tools that operate with limited or no prior knowledge about the application domain. These earlier efforts include XTRACT, a tool that recovers collocational restrictions between words that has been licensed to more than thirty sites worldwide (Smadja, F., 1993, J. Comp. Ling. 19:143-177), CHAMPOLLION, a system that retrieves bilingual mappings between words and phrases in parallel texts from different languages (Smadja, F. et al. 1996, J. Computational Linguistics 22:1-38), and a system that automatically aligns noisy, semi-parallel texts from different languages (Fung, P. and McKeown, K.R., 1997, Machine Translation 11:23-29).

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in genomics journal articles. To enable access to information in textual form, the natural language processing system of the present invention provides a method for extracting and structuring information found in the literature in a form appropriate for subsequent applications. Specifically, the present invention provides for the generation of specialized databases containing information on gene/protein structure, function and regulatory interactions based on the retrieval of such information from research articles and databases, and computer representation of such information in a manner that allows efficient access to the extracted information.

The invention further provides for the use of the specialized databases for identifying novel genes based on detection of sequence similarities and domain/motif matches between genes/proteins, computation and interpretation of phylogenetic trees for multigene families, and analysis of homologous regulatory networks. The methods of the invention are based on the observation that functionally similar regulatory systems are generated during evolution by genetic duplication of ancestral genes. Thus, a comparison of homologous/similar networks within the same organism and between different species will allow the identification of genes absent in one of the systems under comparison. In this way genes that contribute to the phenotype of a specific disease associated with a particular biological system under analysis may be identified.

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2. BACKGROUND OF THE INVENTION

2.1. <u>NATURAL LANGUAGE PROCESSING</u>

Researchers working in molecular biology must constantly consider the information present in the literature relating to their regulatory systems of interest and the genes and proteins that operate within those systems. Unfortunately, to remain upto-date on the relevant literature, the researcher is required to perform laborious reading and manual integration of research articles, each of which may address a narrow subject. Therefore, technology that enables rapid retrieval of information from literature and manipulation of derived functional data should have a dramatic effect on the accesss of the researcher to important facts and ultimately should facilitate the discovery of novel human genes.

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GENE DISCOVERY THROUGH COMPARISONS OF NETWORKS OF STRUCTURAL AND FUNCTIONAL RELATIONSHIPS AMONG KNOWN GENES AND PROTEINS

SPECIFICATION

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The invention described herein was funded in part by a grant from the National Library of Medicine, namely, Grant Number's LM06274 and LM05627. The United States Government may have certain rights to the invention. The present specification contains a computer program listing which appears as a microfiche Appendix H.

STATEMENT REGARDING MATERIAL SUBJECT TO COPYRIGHT

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An appendix containing source code listing utilized in practicing an exemplary embodiment of the invention is included as part of the Specification.

1. <u>INTRODUCTION</u>

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The present invention relates to methods for identifying novel genes comprising: (i) generating one or more specialized databases containing information on gene/protein structure, function and/or regulatory interactions; and (ii) searching the specialized databases for homology or for a particular motif and thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest.

The present invention relates to natural language processing and extraction of relational information associated with genes and proteins that are found

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(54) Title: GENE DISCOVERY THROUGH COMPARISONS OF NETWORKS OF STRUCTURAL AND FUNCTIONAL RELATION-SHIPS AMONG KNOWN GENES AND PROTEINS

(57) Abstract

The present invention relates to methods for identifying novel genes comprising: (i) generating one or more specialized databases containing information on gene/protein structure, function and/or regulatory interactions; and (ii) searching the specialized databases for homology or for a particular motif and thereby identifying a putative novel gene of interest. The invention may further comprise performing simulation and hypothesis testing to identify or confirm that the putative gene is a novel gene of interest. The present invention also relates to natural language processing and extraction of relational information associated with genes and proteins that are found in genomics journal anticles. To enable access to information in textual form, the natural language processing system of the present invention provides a method for extracting and structuring information found in the literature in a form appropriate for subsequent applications.

```
synw(disengaged, ved).
synw(disengaged, ven).
synw(disengagement, n).
synw(disengages, vp).
synw(disengaging,n).
synw(disengaging, ving).
synw(divide, v).
synw(divide, vp).
synw(divided, ved).
synw(divided, ven).
synw(divides, vp).
synw(dividing,n).
synw(dividing, ving).
synw(division,n).
synw(dying,n).
synw(dying, ving).
synw (enhance, v).
synw(enhance, vp).
synw (enhanced, ved) .
synw (enhanced, ven).
synw(enhancement,n).
synw (enhances, vp).
synw (enhancing, n).
synw(enhancing, ving).
synw(express, v).
synw (express, vp).
synw(expressed, ved).
synw (expressed, ved) .
synw(expressed, ven).
synw (expresses, vp).
synw(expressing,n).
synw(expressing,n).
synw(expressing, ving).
synw(expression,n).
synw(generate, v).
synw (generate, vp).
synw (generated, ved).
synw(generated, ven).
synw(generates, vp).
synw (generating, n).
synw(generating, ving).
synw(generation,n).
synw(hew, v).
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```
synw(hew, vp).
synw(hewed, ved).
synw(hewed, ven).
synw(hewing, n).
synw(hewing, ving).
synw(hews, vp).
synw(hinder, v).
synw(hinder, vp).
synw(hindered, ved).
synw(hindered, ven).
synw(hindering,n).
synw(hindering, ving)...
synw(hinders, vp).
synw(hindrance,n).
synw(inactivate, v).
synw(inactivate, vp).
synw(inactivated, ved).
synw(inactivated, ven).
synw(inactivates, vp).
synw(inactivating,n).
synw(inactivating, ving).
synw(inactivation, n).
synw(incite, v).
synw(incite, vp).
synw(incited, ved).
synw(incited, ven).
synw(incitement, n).
synw(incites, vp).
synw(inciting,n).
synw(inciting, ving).
synw(induce, v).
synw(induce, vp).
synw(induced, ved).
synw(induced, ven).
synw(induces, vp).
synw(inducing,n).
synw(inducing, ving).
synw(induction, n).
synw(influence,n).
synw(influence, v).
synw(influence, vp).
synw(influenced, ved).
synw(influenced, ven).
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```
synw(influences, vp)...
synw(influencing,n).
synw(influencing, ving). % ?
synw(inhibit, v).
synw(inhibit, vp).
synw(inhibited, ved).
synw(inhibited, ven).
synw(inhibiting,n).
synw(inhibiting, ving).
synw(inhibition,n).
synw(inhibits, vp).
synw(initiate, v).
synw(initiate, vp).
synw(initiated, ved).
synw(initiated, ven).
synw(initiates, vp).
synw(initiating,n).
synw(initiating, ving).
synw(initiation, vp).
synw(instigate, v).
synw(instigate, vp).
synw(instigated, ved).
synw(instigated, ven).
synw(instigates, vp).
synw(instigating,n).
synw(instigating, ving).
synw(instigation,n).
synw(interact,v).
synw(interact, vp).
synw(interacted, ved).
synw(interacted, ven).
synw(interacting,n).
synw(interacting, ving).
synw(interaction,n).
synw(interactions,n).
synw(interacts, vp).
synw(join ,vp).
synw(join, v).
synw(joined, ved).
synw(joined, ven).
synw(joining,n).
synw(joining, ving).
synw(joins, vp).
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synw(juncture, n).
synw(liberate, v).
synw(liberate, vp).
synw(liberated, ved).
synw(liberated, ven).
synw(liberates, vp).
synw(liberating,n).
synw(liberating, ving).
synw(liberation,n).
synw(limit,v).
synw(limit, vp).
synw(limitation, n). . .
synw(limited, ved).
synw(limited, ven).
synw(limiting,n).
synw(limiting, ving).
synw(limits, vp).
synw(link,n).
syrw(link,v).
synw(link, vp).
synw(linked, ved).
synw(linked, ven).
synw(linking,n).
synw(linking, ving).
synw(links, vp).
synw(mediate, v).
synw(mediate, vp).
synw(mediated, ved).
synw(mediated, ven).
synw(mediates, vp).
synw(mediating,n).
synw(mediating, ving).
synw(mediation,n).
synw(methylate, vp).
synw(methylate,v).
synw(methylated, ved).
synw(methylated, ven ).
synw(methylates, vp).
synw(methylating,n).
synw(methylating, ving).
synw(methylation, n).
synw(modification,n).
synw(modified, ved).
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synw(modified, ven).
synw(modifies, vp).
synw(modify, v).
synw(modify, vp).
synw(modifying,n).
synw(modifying, ving).
synw(mutate, v).
synw(mutate, vp).
synw(mutated, ved).
synw(mutated, ven).
synw(mutates, vp).
synw(mutating,n).
synw(mutating, ving).
synw(mutation,n).
synw(overexpress, v).
synw(overexpress, vp).
synw(overexpressed, ved).
synw (overexpressed, ven) .
synw(overexpresses, vp).
synw(overexpressing,n).
synw(overexpressing, ving).
synw(overexpression, n).
synw(pair,v).
synw(pair, vp).
synw(paired, ved).
synw(paired, ven).
synw(pairing,n).
synw(pairing, ving).
synw(pairs, vp).
synw(phosphorylate,n).
synw(phosphorylate, vp).
synw(phosphorylated, ved).
synw(phosphorylated,ven).
synw(phosphorylates, vp).
synw(phosphorylating,n).
synw(phosphorylating,ving).
synw(phosphorylation, n).
synw(promote, v).
synw(promote, vp).
synw(promoted, ved).
synw(promoted, ven).
synw(promotes, vp).
synw(promoting,n).
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synw(promoting, ving).
synw(promotion, n).
synw(prompt, n).
synw(prompt, v).
synw(prompt, vp).
synw(prompted, ved).
synw(prompted, ven).
synw(prompting,n).
synw(prompting, ving).
synw(prompts, vp).
synw(react, v).
synw(react, vp).
synw(reacted, ved).
synw(reacted, ven).
synw(reacting,n).
synw(reacting, ving).
synw(reaction,n).
synw(reacts, vp).
synw(regulate, v).
synw(regulate, vp).
synw(regulated, ved).
synw(regulated, ven).
synw(regulates, vp).
synw(regulating, n).
synw(regulating, ving).
synw(regulation, n).
synw(release, n).
synw(release, v).
synw(release, vp).
synw(released, ved).
synw(released, ven).
synw(releases, vp).
synw(releasing, n).
synw(releasing, ving).
synw(removal,n).
synw(remove, v).
synw (remove, vp).
synw(removed, ved).
synw(removed, ven).
synw(removes, vp).
synw(removing,n).
synw(removing, ving).
synw(replace, v).
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```
synw(replace, vp).
synw(replaced, ved).
synw(replaced, ven).
synw(replacement, n).
synw(replaces, vp).
synw(replacing,n).
synw(replacing, ving).
synw(repress, vp).
synw(repress, v).
synw(repressed, ved).
synw(repressed, ven).
synw(represses, vp).
synw(repressing,n).
synw(repressing, ving).
synw(repression, n).
synw(require, v).
synw(require, vp).
synw(required, ved).
synw(required, ven).
synw(requirement,n).
synw(requires, vp).
synw(requiring, n).
synw(requiring, ving).
synw(restrain, vp).
synw(restrain,v).
synw(restrained, ved).
synw(restrained, ven).
synw(restraining,n).
synw(restraining, ving).
synw(restrains, vp).
synw(restraint, n).
synw(sensitization, n).
synw(sensitize, vp).
synw(sensitize, v).
synw(sensitized, ved).
synw(sensitized, ven).
synw(sensitizes, vp).
synw(sensitizing,n).
synw(sensitizing, ving).
synw(separate, v).
synw(separate, vp).
synw(separated, ved).
synw(separated, ven).
```

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```
synw(separates, vp).
synw(separating, n).
synw(separating, ving).
synw(separation, n).
synw(sever, v).
synw(sever, vp).
synw(severance, n).
synw(severed, ved).
synw(severed, ven).
synw(severing,n).
synw(severing, ving).
synw(severs, vp).
synw(signal, v).
synw(signal, vp).
synw(signaled, ved).
synw(signaled, ved).
synw(signaled, ven).
synw(signaling, n).
synw(signaling, ving).
synw(signals, vp).
synw(split,n).
synw(split,v).
synw(split, ved).
synw(split, ven).
synw(split, vp).
synw(splits, vp).
synw(splitting,n).
synw(splitting, ving).
synw(stimulate, v).
synw(stimulate, vp).
synw(stimulated, ved).
synw(stimulated, ven).
synw(stimulates, vp).
synw(stimulating,n).
synw(stimulating, ving).
synw(stimulation, n).
synw(substitute, v).
synw(substitute, vp).
synw(substituted, ved).
synw(substituted, ven).
synw(substitutes, vp).
synw(substituting,n).
synw(substituting, ving).
```

```
synw(substitution,n).
synw(suppress, vp).
synw(suppress, v).
synw(suppressed, ved).
synw(suppressed, ven) . .
synw(suppresses, vp).
synw(suppressing,n).
synw(suppressing, ving).
synw(suppression, n).
synw(tie,n).
synw(tie, v).
synw(tie, vp).
synw(tied, ved).
synw(tied, ven).
synw(ties, vp).
synw(transcribe, v).
synw(transcribe, vp).
synw(transcribed, ved).
synw(transcribed, ven).
synw(transcribes, vp).
synw(transcribing,n).
synw(transcribing, ving).
synw(transcription,n).
synw(tying, n).
synw(tying, ving).
synw (ubiquitinization, n) .
synw(ubiquitinize, v).
synw(ubiquitinize, vp).
synw(ubiquitinized, ved).
synw(ubiquitinized, ven).
synw(ubiquitinizes, vp).
synw (ubiquitinizing, n).
synw(ubiquitinizing, ving).
synw(urge, n).
synw(urge, v).
synw(urge, vp).
synw(urged, ved).
synw(urged, ven).
synw(urges, vp).
synw(urging, n).
synw(urging, ving).
% the following are verbs connected with complexes
synw(form, v). .
```

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```
synw(form, vp).
synw(forms, vp).
synw(formed, ved).
synw(formed, ven).
synw(forming,n).
synw(formation,n).
synw(assemble, v).
synw(assemble, vp).
synw(assembles, vp).
synw(assembled, ved).
synw(assembled, ven).
synw(assembling,n).
synw(assembly,n).
synw(dissassemble, v).
synw(dissassemble, vp).
synw(dissassembles, vp).
synw(dissassembled, ved).
synw(dissassembled, ven).
synw(dissassembling,n).
synw(dissassembly,n).
synw(dissociate, v).
synw(dissociate, vp).
synw(dissociates, vp).
synw(dissociated, ved).
synw(dissociated, ven).
synw (dissociating, n).
synw(dissociation,n).
synw(recruit, v).
synw(recruit, vp).
synw(recruits, vp).
synw(recruited, ved).
synw(recruited, ven).
synw (recruiting, n).
synw(recruitment,n).
```

```
% lexsemact.pat
% revised March 17, 2000
             SEMANTIC LEXICON OF ACTIONS
응응응응응응용
% For genomics - the grammar tests for semantic and syntactic cate
% separately for action type of categories; for substances the lex
ical
% entries are the same as in the medical area
% action type phrases have two entries: a semantic entry and a syn
tactic entry
% This lexicon contains the semantic entries for words and phrases
% semp is a lexical entry for phrasal lexicon
% semp(+Word1,+Sem,+Wordlist,+Targetform,+Features)
% semp specifies a semantic lexical definition for the genomics li
terature
% semp is equivalent to the predicate "phrase" in the medical area
% semp: Word1 is first word of phrase, Sem is semantic category
% semp: Wordlist is list of words in phrase, Targetform is output
form
% semp: Features is a list of 2 elements or the atom "def" represe
nting defaul
% semp: Features 1st element is rev or nrev meaning reversed or no
t reversed
% semp: Features 2nd element is a # specifying number of arguments
 for action
% semp: Features = def is equivalent to a list = [nrev,2]
% in case action has 1 argument, use [1, ]
%semw is a lexical entry for single word
% semw(+Word,+Sem,+Targetform,+Features)
% semw: the arguments are the same as for semp except there is no
Wordlist
웅응응응응용응용
:- multifile(semp/5).
:- multifile(semw/4).
semp(account, cause, [account, for], cause, [def]).
semp(accounted, cause, [accounted, for], cause, [def]).
```

Appendix C

```
semp(accounting, cause, [accounting, for], cause, [def]).
semp(accounts, cause, [accounts, for], cause, [def]).
           attach, [add, up], attach, [def]).
semp(added,
             attach, [added, up], attach, [def]).
semp(adds,
            attach, [adds, up], attach, [def]).
semp(are, cause, [are, a, means, of, producing], cause, [def]).
semp(are,cause,[are,due,to],cause,[2,rev]).
semp(as, cause, [as, a, result, of], cause, [2, rev]).
semp(attributable, cause, [attributable, to], cause, [2, rev]).
semp(attributed, cause, [attributed, to], cause, [2, rev]).
semp(based, cause, [based, on], cause, [2, rev]).
semp(based, cause, [based, upon], cause, [2, rev]).
semp(because, cause, [because, of], cause, [2, rev]).
semp(convey, signal, [conveys,a, signal], signal, [def]).
semp(conveyed, signal, [conveyed,a, signal], signal, [def]).
semp(conveying, signal, [conveying, a, signal], signal, [def]).
semp(conveys, signal, [conveys,a, signal], signal, [def]).
semp(dissociate, release, [dissociate, from], release, [def]).
semp(dissociated, release, [dissociated, from], release, [def]).
semp(dissociates, release, [dissociates, from], release, [def]).
semp(dissociation, release, [dissociation, from], release, [def]).
semp(down, signal, [down, '-', regulate], signal, [def]).
                   A --> B
regulates B
semp(down, signal, [down, '-', regulated], signal, [def]).
                                                                A down
-regulates B
                    A --> B
semp(down, signal, [down, '-', regulates], signal, [def]).
-regulates B
                     A --> B
semp(down, signal, [down, '-', regulation], signal, [def]).
                                                                A dow
n-regulates B
                    A --> B
semp(due, cause, [due, to, the, fact, that], cause, [2, rev]).
semp(due, cause, [due, to], cause, [2, rev]).
semp(form, attach, [form, complex], attach, [def]).
semp(formation, attach, [formation, of, complex], attach, [def]).
semp(formed, attach, [formed, complex], attach, [def]).
semp(forms, attach, [forms, complex], attach, [def]).
semp(had, cause, [had, an, active, role, in], cause, [def]).
semp(has, cause, [has, an, active, role, in], cause, [def]).
semp(have, cause, [have, an, active, role, in], cause, [def]).
semp(is, cause, [is,a,means,of, producing], cause, [def]).
semp(is, cause, [is, due, to], cause, [2, rev]).
semp(functions, inactivate, [functions, as, a, negative, regulator, of], i
nactivate, [def]).
semp(function,inactivate,[function,as,a,negative,regulator,of],ina
```

```
ctivate, [def]).
semp(lead, cause, [lead, to], cause, [def]).
semp(lead, cause1, [lead, to], cause, [def]).
semp(leading, cause, [leading, to], cause, [def]).
semp(leading, cause, [leading, to], cause, [def]).
semp(leads, cause, [leads,to], cause, [def]).
semp(leads, cause1, [leads, to], cause, [def]).
semp(led, cause, [led, to], cause, [def]).
semp(may, cause, [may, be, responsible, for], cause, [def]).
semp(mediate, signal, [mediate, a, signal], signal, [def]).
                                                                 용À
mediates a signal to B
semp(mediated, signal, [mediated, a, signal], signal, [def]).
A mediates a signal to B
semp(mediates, signal, [mediates, a, signal], signal, [def]).
A mediates a signal to B
semp(mediation, signal, [mediation, of, a, signal], signal, [def]).
    %A mediates a signal to B
semp(n, createbond, [n,'-',acetylate],'N-acetylate',[def]).
semp(n, createbond, [n,'-',acetylated],'N-acetylate',[def]).
semp(n, createbond, [n,'-',acetylates],'N-acetylate',[def]).
semp(n, createbond, [n,'-',acetylation],'N-acetylate',[def]).
semp(n, createbond, [n,'-',acylate],'N-acylate',[def]).
semp(n, createbond, [n,'-',acylated],'N-acylate',[def]).
semp(n, createbond, [n,'-',acylates],'N-acylate',[def]).
semp(n, createbond, [n,'-',acylation],'N-acylate',[def]).
semp(n, createbond, [n,'-',glycosylate],'N-glycosylate',[def]).
semp(n, createbond, [n,'-',glycosylated],'N-qlycosylate',[def]).
semp(n, createbond, {n,'-',glycosylates},'N-glycosylate',[def]).
semp(n, createbond, [n,'-',glycosylation],'N-glycosylate',[def]).
semp(n,breakbond, [n,'-',terminal,proteolysis],'n-terminal proteoly
sis', [def]).
semp(o, createbond, [o,'-',glycosylate], 'O-glycosylate', [def]).
semp(o, createbond, [o,'-',glycosylated], 'O-glycosylate', [def]).
semp(o, createbond, [o,'-',glycosylates], '0-glycosylate', [def]).
semp(o, createbond, [o,'-',glycosylation], 'O-glycosylate',[def]).
semp(only,time,[only,after],'only after',[2,rev]).
semp(prolyl, createbond, [prolyl,'-',4,'-',hydroxylate],
                   'prolyl-4-hydroxylate', [def]).
semp(prolyl, createbond, [prolyl,'-',4,'-',hydroxylated],
                     'prolyl-4-hydroxylate', [def]).
semp(prolyl, createbond, [prolyl,'-',4,'-',hydroxylates],
                'prolyl-4-hydroxylate', [def]).
semp(prolyl, createbond, [prolyl,'-',4,'-',hydroxylation],
```

```
'prolyl-4-hydroxylate', [def]).
semp(result, cause, [result, from], cause, [2, rev]).
semp(result, cause, [result, in], cause, [def]).
semp(resulted, cause, [resulted, from], cause, [2, rev]).
semp(resulted, cause, [resulted, in], cause, [def]).
semp(resulting, cause, [resulting, from], cause, [2, rev]).
semp(resulting, cause, [resulting, in], cause, [def]).
semp(results, cause, [results, from], cause, [2, rev]).
semp(results, cause, [results, in], cause, [def]).
semp(set, release, [set, free], release ,[def]).
semp(set, release, [set, free], release, [def]).
semp(sets, release, [sets, free], release, [def]).
semp(setting, release, [setting, free], release , [def]).
semp(suppress, inactivate, [suppress, activity, of], inactivate, [
def]).
semp(suppressed, inactivate, [suppressed, activity, of], inactivat
e, [def]).
semp(suppresses, inactivate, [suppresses, activity, of], inactivat
semp(suppression, inactivate, [suppression, of, activity, of], inac
tivate, [def]).
semp(switch, activate, [switch, on, the, activity, of],
, [def]).
semp(switched,
                 activate, [switched, on, the, activity, of],
vate, [def]).
semp(switches,
                 activate, [switches, on, the, activity, of], acti
vate, [def]).
semp(up, signal, [up, '-', regulate], signal, [2, rev]). % A up-regul
ates B B --> A
semp(up, signal, [up, '-', regulated], signal, [2, rev]).
semp(up, signal, [up, '-', regulates], signal, [2, rev]).
semp(up, signal, [up, '-', regulation], signal, (2, rev]).
semp(was, cause, [was,a,means,of, producing], cause, [def]).
semp(was, cause, [was, due, to], cause, [2, rev]).
semp(were, cause,[were,a,means,of, producing],cause,[def]).
semp(were, cause, [were, due, to], cause, [2, rev]).
semw(acetylate, createbond, acetylate,[def]).
semw(acetylated, createbond, acetylate, [def]).
semw(acetylates, createbond, acetylate, [def]).
semw(acetylation, createbond, acetylate,[def]).
semw(activate, activate, activate, [def]).
semw(activated, activate, activate, [def]).
semw(activates, activate, activate, [def]).
```

```
semw(activation, activate, activate, [def]).
semw(add, attach, attach, [def]).
semw(added, attach, attach, [def]).
semw(addition, attach,
                         attach, [def]).
semw(adds, attach, attach, [def]).
semw(after, time, after, [2, rev]).
                                     % temporal relations
semw(aggregate ,attach,attach,[def]).
semw(aggregated ,attach,attach,[def]).
semw(aggregates, attach, attach, [def]).
semw(aggregation ,attach,attach,[def]).
semw(arrest, inactivate, inactivate, [def]).
semw(arrested, inactivate, inactivate, [def]).
semw(arrests, inactivate, inactivate, [def]).
semw(associate, attach, attach, [def]).
semw(associated, attach, attach, [def]).
semw(associates, attach, attach, [def]).
semw(association, attach, attach, [def]).
semw(attach, attach, attach, [def]).
semw(attached ,attach,attach,[def]).
semw(attaches, attach, attach, [def]).
semw(attachment, attach, attach, [def]).
semw(bind, attach, attach, [def]).
semw(binding,attach, attach, [def]).
semw(binds, attach, attach, [def]).
semw(block, inactivate, inactivate, [def]).
semw(blocked, inactivate, inactivate, [def]).
semw(blocking, inactivate, inactivate, [def]).
semw(blocks, inactivate, inactivate, [def]).
semw(bound, attach, attach, [def]).
                        'break bond', [def]).
semw(break, breakbond,
semw(breakage, breakbond,
                            'break bond', [def]).
semw(breaks, breakbond,
                          'break bond', [def]).
semw(broke, breakbond,
                         'break bond', [def]).
semw(broken, breakbond, 'break bond', [def]). % case without break
bond
semw(catalyzation, promote, catalyze, [def]).
semw(catalyze, promote, catalyze, [def]).
semw(catalyzed, promote, catalyze, [def]).
semw(catalyzes,promote,catalyze,[def]).
semw(catalyzing,promote, catalyze,[def]).
semw(cause, cause, cause, [def]).
semw(caused, cause, cause, [def]).
semw(causes, cause, cause, [def]).
```

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semw(cleavage, breakbond, 'break bond', [def]).
semw(cleave, breakbond,
                         'break bond', [def]).
semw(cleaved, breakbond, 'break bond', [def]).
semw(cleaves, breakbond,
                          'break bond', [def]).
semw(coimmunoprecipitate, attach, attach, [def]).
semw(coimmunoprecipitated ,attach,attach,[def]).
semw(coimmunoprecipitates, attach, attach, [def]).
semw(coimmunoprecipitation ,attach,attach,[def]).
semw(combination ,attach,attach,[def]).
semw(combine ,attach,attach,[def]).
semw(combined ,attach,attach,[def]).
semw(combines, attach, attach, [def]).
semw(conjugate ,attach,attach,[def]).
semw(conjugated ,attach,attach,[def]).
semw(conjugates, attach, attach, [def]).
semw(conjugation ,attach,attach,[def]).
semw(connect ,attach,attach,[def]).
semw(connected ,attach,attach,[def]).
semw(connection ,attach,attach,[def]).
semw(connects, attach, attach, [def]).
semw(constrain, inactivate, inactivate, [def]).
semw(constrained, inactivate, inactivate, [def]).
semw(constrains, inactivate, inactivate,[def]).
semw(constraint, inactivate, inactivate, [def]).
semw(coprecipitate, attach, attach, [def]).
semw(coprecipitated, attach, attach, [def]).
semw(coprecipitates, attach, attach, [def]).
semw(coprecipitation ,attach,attach,[def]).
semw(copurification ,attach,attach,[def]).
semw(copurified ,attach,attach,[def]).
semw(copurifies, attach, attach, [def]).
semw(copurify ,attach,attach,[def]).
semw(couple ,attach,attach,[def]).
semw(coupled, attach, attach, [def]).
semw(couples, attach, attach, [def]).
semw(cut, breakbond, 'break bond',[def]). % leave breakbond onl
y?
semw(cuts, breakbond, 'break bond', [def]).
semw(deactivate, inactivate, inactivate, [def]).
semw(deactivated, inactivate, inactivate, [def]).
semw(deactivates, inactivate, inactivate, [def]).
semw(deactivation, inactivate, inactivate, [def]).
semw(death, process, death,[1]).
```

```
semw(demethylate, breakbond, demethylate, [def]).
semw(demethylated, breakbond, demethylate, [def]).
semw(demethylates, breakbond, demethylate, [def]).
semw(demethylation, breakbond, demethylate, [def]).
semw(dephosphorylate, breakbond,dephosphorylate,[def]).
semw(dephosphorylated, breakbond,dephosphorylate,[def]).
semw(dephosphorylates, breakbond,dephosphorylate,[def]).
semw(dephosphorylation, breakbond,dephosphorylate,[def]).
semw(die, process, death,[1]).
semw(died, process, death,[1]).
semw(dies, process, death, [1]).
semw(disassemble, release, release, [def]).
semw(disassembled, release, release, [def]).
semw(disassembles, release, release, [def]).
semw(disassembly, release, release, [def]).
semw(discharge, release, release, [def]).
semw(discharged, release, release, [def]).
semw(discharges, release, release, [def]).
semw(disengage, release, release, [def]).
semw(disengaged, release, release, [def]).
semw(disengagement, release, release, [def]).
semw(disengages, release, release, [def]).
semw(divide, breakbond,
                         'break bond', [def]).
semw(divided, breakbond,
                           'break bond', [def]).
semw(divides, breakbond,
                          'break bond', [def]).
semw(division, breakbond,
                            'break bond', [def]).
semw(dying, process, death,[1]).
semw(enhance, promote, promote, [def]).
semw(enhanced,promote,promote,[def]).
semw(enhancement, promote, promote, [def]).
semw(enhances, promote, promote, [def]).
semw(enhancing, promote, promote, [def]).
semw(express, generate, express, [def]). % can have either 1 or 2 ar
quments
semw(expressed, generate, express, [def]).
semw(expresses, generate, express, [def]).
semw(expressing, generate, express, [def]).
semw(expression, generate, express, [def]).
semw(generate,generate,generate,[def]).
semw(generated,generate,generate,[def]).
semw(generates, generate, generate, [def]).
semw(generating,generate,generate,[def]).
semw(generation,generate,generate,[def]).
```

```
semw(hew, breakbond,
                     'break bond', [def]).
semw(hewed, breakbond, 'break bond', [def]).
semw(hews, breakbond,
                       'break bond', [def]).
semw(hinder, inactivate, inactivate, [def]).
semw(hindered, inactivate, inactivate, [def]).
semw(hinders, inactivate, inactivate, [def]).
semw(hindrance, inactivate, inactivate, [def]).
semw(inactivate, inactivate, inactivate, [def]).
semw(inactivated, inactivate, inactivate, [def]).
semw(inactivates, inactivate, inactivate, [def]).
semw(inactivation, inactivate, inactivate, [def]).
semw(incite, activate, activate, [def]).
semw(incited, activate, activate, [def]).
semw(incitement, activate, activate, [def]).
semw(incites, activate, activate, [def]).
semw(induce, activate, activate, [def]).
semw(induced, activate, activate, [def]).
semw(induces, activate, activate, [def]).
semw(induction, activate, activate, [def]).
semw(influence, activate, activate, [def]).
semw(influenced, activate, activate, [def]).
semw(influences, activate, activate, [def]).
semw(influencing, activate, activate,[def]).
semw(inhibit, inactivate, inactivate,[def]).
semw(inhibited, inactivate, inactivate, [def]).
semw(inhibition, inactivate, inactivate, [def]).
semw(inhibits, inactivate, inactivate, [def]).
semw(initiate, activate, activate, [def]).
semw(initiated, activate, activate, [def]).
semw(initiates, activate, activate, [def]).
semw(initiattion, activate, activate, [def]).
semw(instigate, activate, activate, [def]).
semw(instigated, activate, activate, [def]).
semw(instigates, activate, activate, [def]).
semw(instigation, activate, activate, [def]).
semw(interact, interact, interact, [def]).
semw(interacted, interact, interact, [def]).
semw(interaction, interact, interact, [def]).
semw(interactions, interact, interact, [def]).
semw(interacts, react, interact, [def]).
semw(join ,attach,attach,[def]).
semw(joined ,attach, attach,[def]).
semw(joining, attach, attach, [def]).
```

```
semw(joins, attach, attach, [def]).
semw(juncture, attach, attach, [def]).
semw(liberate, release, release, [def]).
semw(liberated, release, release, [def]).
semw(liberates, release, release, [def]).
semw(liberation, release, release, [def]).
semw(limit, inactivate, inactivate, [def]).
semw(limitation, inactivate, inactivate, [def]).
semw(limited, inactivate, inactivate, [def]).
semw(limits, inactivate, inactivate, [def]).
semw(link, attach, attach, [def]).
semw(linked, attach, attach, [def]).
semw(linking, attach,attach,[def]).
semw(links,attach, attach,[def]).
semw(mediate, promote, promote, [def]).
semw(mediated, promote, promote, [def]).
semw(mediates, promote, promote, [def]).
semw(mediation, promote, promote, [def]).
semw(methylate, createbond, methylate,[def]).
semw(methylated, createbond, methylate, [def]).
semw (methylates, createbond, methylate, [def]).
semw(methylation, createbond, methylate,[def]).
semw(modification, modify, modify, [def]).
semw(modified, modify, modify, [def]).
semw (modifies, modify, modify, [def]).
semw (modify, modify, modify, [def]).
semw(modifying, modify, modify, [def]).
semw(mutate, modify, mutate, [1]).
semw(mutated, modify, mutate, [1]).
semw(mutates, modify, mutate, [1]).
semw(mutating, modify, mutate, [1]).
semw (mutation, modify, mutate, [1]).
semw(overexpressed, generate, overexpress, [def]).
semw(overexpresses, generate, overexpress, [def]).
semw(overexpressing, generate, overexpress, [def]).
semw(overexpress, generate, express, [def]).
semw(overexpression, generate, overexpress, [def]).
semw(pair, attach, attach, [def]).
semw(paired, attach, attach, [def]).
semw(pairing,attach,
                       attach, [def]).
semw (pairs, attach,
                     attach, [def]).
semw(phosphorylate, createbond, phosphorylate,[def]).
semw(phosphorylated, createbond, phosphorylate,[def]).
```

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semw(phosphorylates, createbond, phosphorylate,[def]).
semw(phosphorylation, createbond, phosphorylate,[def]).
semw(precede, cause, cause, [def]).
semw(preceded, cause, cause, [def]).
semw(precedes, cause, cause, [def]).
semw(preceding, cause, cause, [def]).
semw(promote, promote, [def]).
semw(promoted, promote, [def]).
semw(promotes, promote, promote, [def]).
semw(promotion, promote, promote, [def]).
semw(prompt, activate, activate, [def]).
semw(prompted, activate, activate, [def]).
semw(prompting, activate, activate, [def]).
semw(prompts, activate, activate, [def]).
semw(react, react, react, [def]).
semw(reacted, react, react, [def]).
semw(reaction, react, react, [def]).
semw(reactions, react, react, [def]).
semw(reacts, react, [def]).
semw(regulate, signal, signal, [def]).
semw(regulated, signal, signal, [def]).
                                             % B is regulated by
   A --> B
semw(regulates, signal, signal, [def]).
semw(regulation, signal, signal, [def]).
semw(release, release, [def]).
semw(released, release, release, [def]).
semw(releases, release, release, [def]).
semw(removal, breakbond, 'break bond ',[def]).
semw(remove, breakbond, 'break bond ',[def]).
semw(remove, breakbond, 'break bond ', [def]).
semw(removes, breakbond, 'break bond ', [def]).
semw(replace, substitute, substitute, [def]).
semw(replaced,
               substitute, substitute, [def]).
semw(replacement, substitute, substitute, [def]).
semw(replaces, substitute, substitute, [def]).
semw(repress, inactivate, inactivate, [def]).
semw(repressed, inactivate, inactivate, [def]).
semw(represses, inactivate, inactivate, [def]).
semw(repression, inactivate, inactivate, [def]).
semw(require, cause, cause, [2, rev]).
semw(required, cause, cause, [2, rev] ).
semw(requirement, cause, cause, [2,rev]).
semw(requires, cause, cause, [2, rev] ).
```

```
semw(requiring, cause, cause, [2, rev]).
semw(restrain, inactivate, inactivate, [def]).
semw(restrained, inactivate, inactivate, [def]).
semw(restrains, inactivate, inactivate, [def]).
semw(restraint, inactivate, inactivate,[def]).
semw(sensitization, activate, activate, [def]).
semw(sensitize, activate, activate, [def]).
semw(sensitized, activate, activate, [def]).
semw(sensitizes, activate, activate, [def]).
semw(separate, breakbond, 'break bond', [def]).
semw(separated, breakbond, 'break bond', [def]).
semw(separates, breakbond,
                            'break bond', [def]).
semw(separation, breakbond,
                             'break bond', [def]).
semw(sever, breakbond,
                       'break bond', [def]).
semw(severance, breakbond,
                            'break bond', [def]).
semw(severed, breakbond,
                           'break bond', [def]).
semw(severs, breakbond,
                          'break bond', [def]).
semw(signal, signal, [def]).
semw(signaled, signal, signal, [def]).
semw(signaling, signal, signal, [def]).
semw(signals, signal, signal, [def]).
semw(split, breakbond, 'break bond',[def]).
semw(splits, breakbond,
                        'break bond', [def]).
semw(splitting, breakbond, 'break bond', [def]).
semw(stimulate, activate, activate, [def]).
semw(stimulated, activate, activate, [def]).
semw(stimulates, activate, activate, [def]).
semw(stimulation, activate, activate, [def]).
semw(substitute, substitute, substitute, [def]).
semw(substituted, substitute, substitute, [def]).
semw(Substitutes, substitute, substitute, [def]).
semw(substitution, substitute, substitute, [def]).
semw(suppress, inactivate, inactivate, [def]).
semw(suppressed, inactivate, inactivate, [def]).
semw(suppresses, inactivate, inactivate, [def]).
semw(suppression, inactivate, inactivate, [def]).
semw(tie,attach,attach,[def]).
semw(tied, attach, attach, [def]).
semw(ties, attach, attach, [def]).
semw(transcribe,generate,transcribe,[def]).
semw(transcribed,generate,transcribe,[def]).
semw(transcribes,generate,transcribe,[def]).
semw(transcribing,generate,transcribe,[def]).
```

```
semw(transcription, generate, transcribe, [def]).
semw(ubiquitinize, createbond, ubiquitinize, [def]).
semw(ubiquitinize, createbond, ubiquitinize, [def]).
semw(ubiquitinized, createbond, ubiquitinize, [def]).
semw(ubiquitinizes, createbond, ubiquitinize, [def]).
semw(urge, activate, activate, [def]).
semw(urge, activate, activate, [def]).
semw(urged, activate, activate, [def]).
semw(urges, activate, activate, [def]).
semw(urging, activate, activate, [def]).
semw(form, attach, attach, [def]).
semw(forms, attach, attach, [def]).
semw(formed, attach, attach, [def]).
semw(forming, attach, attach, [def]).
semw(formation, attach, attach, [def]).
semw(assemble, attach, attach, [def]).
semw(assembles, attach, attach, [def]).
semw(assembled, attach, attach, [def]).
semw(assembling, attach, attach, [def]).
semw(assembly, attach, attach, [def]).
semw(dissassemble, release, release, [def]).
semw(dissassembles, release, release, [def]).
semw(dissassembled, release, release, [def]).
semw(dissassembling, release, release, [def]).
semw(dissassembly, release, release, [def]).
semw(dissociate, release, release, [def]).
semw(dissociates, release, release, [def]).
semw(dissociated, release, release, [def]).
semw(dissociating, release, release, [def]).
semw(dissociation, release, release, [def]).
semw(recruit, attach, attach, [def]).
semw(recruits, attach, attach, [def]).
semw(recruited, attach, attach, [def]):.
semw(recruiting, attach, attach, [def]).
semw(recruitment, attach, attach, [def]).
```

```
% edited Genome grammar - adapted from MedLEE's grammar for use with MedLEE
% this is to be used along with the genomics lexicon of substances, actions,
   and relations.
% revised March 16, April 5, 2000
% adjusted for tagged input
:- multifile(wdef/3).
:- multifile (phrase/5).
Written by Carol Friedman for the MedLEE System
¥
¥
     Queens College of the City University of New York
* Highest Level Predicate - sem_sent - 1st arg. is target structure
                                  - 2nd arg. is a list of words in sentence%
                                  - 3rd arg. is '[]'
* Target structure: a frame or set of connected frames:
          the frame describes an action or several related actions;
          an action frame is a list consisting of the symbol 'action'
          followed by the code for the action and arguments.
¥
          The arguments are either substances or actions;
          each substance slot consists of the name of the type of
          substance followed by the value for the substance;
          the substance slot may contain slots for several substances.
% Examples:
% Blocking of il-2 gene transcription by activated rapl.
% [action, inactivate, [protein, Rap1, [state, active]],
                   [action, transcribe, [x], [gene, interleukin-2]]]
* The adapter protein crkl was associated with both phosphorylated cbl and the*
% guanidine nucleotide-releasing factor c3g.
% (action,attach, (protein,CrkL),
               [relation, and, [protein, Cbl, [state, phosphorylated]],
                          [protein, quanidine nucleotide-releasing factor C3G,
                                               [state,phosphorylated]]] }
fail an unknown predicate
:- unknown(_,fail).
:- op(900, fy, [not,once]). % same priority and type as \+
:- op(700, xfx, [\=,~=]). % same priority and type as = or \approx=
% snoop is generally used to find input string when using a DCG
       the input string is used for constraints
snoop (A, B, A, B) .
sem_sent(P,Semlist,X) -->
       {assert(addstotal(0))},
       sem parse (P, Semlist, X).
sem_parse(Target,Semlist) -->
       sem_patterns(P,Semlist).
sem_parse(Target,Semlist,X) -->
       sem_patterns(P, Semlist),
       sem_endornot(P, Target, X).
sem_parse([failure],_,X,_,_) :-
       addstotal(X).
sem_endornot(P,P,X) --> % P is target if there is an endmark
```

Appendix D

```
sem_endmark,
        \{addstotal(X)\}. % X is number of times reached endmark
sem_endornot(_,_,_,_) :- % did not reach endmark; update count and fail
       uptotal, fail.
sem_endornot(_,[failure],X,_,_) :-
       addstotal(X), % X is number of times reached
% Finding patterns
sem_patterns(F,Semlist) -->
       pattern(F1, Semlist),
       morepattern (R, F2, Semlist), % connected patterns
       {getrelation(R,F1,F2,F)}.
/************************
* The action pattern types are: pattern, nounactionpatt, actpatt, and *
* nounactpatt.
* pattern --> actionarg(A1)
             active or passive verb
             actionarg(A2).
* pattern --> nounactionpatt.
* pattern --> actpatt.
**********
% pattern is saved in a symbol table (st); check for success/failure 1st
Case where pattern is in st and has been successful
pattern(Fmt,_) --> checkst(pattern,_,s,Fmt).
Case where pattern is in st as a failure.
pattern(_,_) --> checkst(pattern, ,f, ), {!, fail}.
% pattern 5: an action pattern with a nominal verb
% Ps1 cleavage by zvad.
% apoptosis-induced cleavage of PS2 by zDEVD.
pattern(F, Semlist) -->
     snoop(S0,S0),
   { \+ checkst(pattern, 5, _, _, S0, _),
    actionchk(Semlist) },
    nounactionpatt(F),
    snoop(S,S),
   { addst(pattern, 5, s, F, S0, S)
% pattern 1: an action/substance acts on an action/substance
the activation of rap1 inhibits the expression of il-2
* rapl functions as a negative regulator of tcr-mediated il-2 gene
* transcription.
pattern(F, Semlist) --> snoop(S0,S0), % S0 is the input string
   { \+ checkst(pattern,1, _,_,S0,_),
     actionchk(Semlist),
    connectchk(Semlist) },
    actionarg(A1),
```

```
connectact (Sem, [v, vp, ved], Target, Features),
     actionarg(A2),
     snoop(S,S), %ending sentence list
   { member(def, Features),
     modlist([A1,A2,Site],Mods);
     member (rev, Features),
     modlist([A2,A1,Site],Mods)),
     frame (F, action, Target, Mods),
     addst(pattern, 1, s, F, SO, S)
   }.
% pattern 2: an action/substance was acted on by an action/substance
t The aggregation of bad was suppressed.
% The aggregation of bad was suppressed by the phosphorylation of jnk.
% Grb2 was associated with Cbl.
% Apoptosis-associated cleavage of endogenous PS1 was blocked by the
% treatment with zVAD.
pattern(F, Semlist) -->
     snoop(S0,S0), % S0 is the input string
    { \+ checkst(pattern, 2, _, _, S0, _),
      actionchk (Semlist),
      connectchk(Semlist) },
      actionarg(A2),
      sem_beterm(_),
                       % was
      connectact (Sem, [ven], Target, Features), %activated
      optbyarg(A1),
      snoop(S,S), %ending sentence list
   { (member(def, Features),
      modlist([A1,A2,Site],Mods);
      member (rev, Features),
      modlist([A2,A1,Site],Mods)),
      frame (F, action, Target, Mods),
      addst(pattern, 2, s, F, S0, S)
   }.
% pattern 3: an action/substance acted on an action/substance
% bad induced phosphorylation of fyn.
% tcr and cd28-mediated il-2 transcription.
pattern(F,Semlist) -->
     snoop(S0,S0),
   { \+ checkst(pattern, 3,_,_,S0,_),
     actionchk (Semlist),
     connectchk(Semlist) },
     actionarg(A1),
                      * substance or basic action
   % optdash,
    % optof.
    actionarg(A2), % had pattern here
     snoop(S,S),
  { (member(def, Features),
    modlist([A1,A2,Site],Mods);
    member (rev, Features),
    modlist([A2,A1,Site],Mods)),
     frame (F, action, Target, Mods),
    addst(pattern, 3, s, F, S0, S)
 1.
```

```
$ pattern 4: a simple action pattern with an active verb.
% Activated Raf-1 phosphorylates MEK-1.
pattern(F, Semlist) -->
     snoop ($0, $0),
     %check that sentence has an action word/phrase
   { \+ checkst(pattern, 4,_,_,S0,_),
     actionchk(Semlist) },
     actpatt(F),
     snoop(S,S),
   { addst(pattern, 4, s, F, S0, S)
  }.
% no more patterns - save failure
pattern(_,_) --> addst(pattern,0,f,_), {!, fail}.
% sem morepattern(-Rel,-P,+Semlist,+S0,+S):
        Rel is a relation and its value frame;
ş.
        P is the remaining patterns, Semlist is the list of semantic classes
        in sentence
% if have a series of ','s, use the relation "and" or "or" if in the nest
% and make that the relation
morepattern(R,F,Semlist) -->
        sem relation(R1, Mod1),
                                 %relation and modifiers
        sem patterns(F, Semlist),
        (Conj2 = and; Conj2 = or), frame(R1, rel, ', ', ), % R1 relation frame
           frame(R,rel,Conj2, ) % value of relation is Conj2
           R1 \succeq [], % where do Type, Value and Mods2 come from?
          frame (R1, Type, Value, Mod2), % get components of original relation
          mergemods (Mod1, Mod2, Mods),
          ( Mods = [], frame(R,rel,Value,[]), !;
            %frame(R,rel,[Value|Mods],[]) % make it rel connector with rel mod
            R = [rel, [Value | Mods]]
          )
         ).
        }.
% no more findings
morepattern([],[], ,S,S).
% actionarg is the argument of pattern
% actionarg is either a substance or a basic action
% actionarg is saved in a symbol table (st); check for success/failure 1st
% Case where actionard is in st and have been successful
actionarg(A) --> checkst(actionarg,_,s,A).
t Case where actionarg is in st as a failure.
actionarg(_) --> checkst(actionarg,_,f;_), {!, fail}.
% actionarg 1: a substance or substances
% Rap1, active Rap1, Cbl and Crkl
actionarg(A) --> snoop(S0,S0), % S0 is the input string
              { \+ checkst(actionarg,1,_,_,S0,_)},
                substances (A),
                snoop(S,S),
              { addst(actionarg,1,s,A,S0,S) }.
```

```
% actionarg 2: a process like apoptosis, or a disease
actionarg(A) --> snoop(S0,S0), % S0 is the input string
              { \+ checkst(actionarg, 2, _, _, 50, _)},
                processpatt (A),
                snoop(S,S),
              { addst(actionarg, 2, s, A, S0, S)
   }.
% actionarg 3: a nominal action pattern
% Etoposide-induced apoptosis.
* Etoposide-induced PS1 cleavage by 2VAD.
actionarg(A) --> snoop(S0,S0), % S0 is the input string
              { \+ checkst(actionarg, 3, _, _, S0, _) },
                nounactionpatt(A),
                snoop(S,S),
                 {addst(actionarg, 3, s, A, S0, S)
% actionarg 4: the object of the nominal action is an actionarg
& Blocking of IL-2 Gene transcription by activated rapl.
actionarg(A) --> snoop(S0,S0), % S0 is the input string
                 { \+ checkst(actionarg, 4 , _, _, SO, _) },
                   action(Sem, [n, ving], Target, Features),
                    [of],
                   actionarg(Al),
                   optbyagent (A2),
                   snoop(S,S),
                 { (member(def, Features),
                   modlist([A1, A2], Mods);
                   member (rev, Features),
                   modlist([A2,A1],Mods)),
                   frame (A, action, Target, Mods),
                   addst(actionarg, 4, s, A, SO, S)
     }.
* no more actionarg - save failure -
actionarg(_) --> addst(actionarg, 0, f, _), {!, fail}.
* nounactionpatt is a nominal action pattern which allows for left and right
1 Il-2 gene transcription mediated by tcr and cd28 was inhibited by rapl.
Activated rap1 functions as a negative regulator of tcr and cd-28-mediated
il 2 transcription.
nounactionpatt is saved in a symbol table (st); check for success/failure 1st
t Case where nounactionpatt is in st and has been successful
nounactionpatt(A) --> checkst(nounactionpatt,_,s,A).
* Case where nounaction patt is in st as a failure.
nounactionpatt(_) --> checkst(nounactionpatt,_,f,_), {!, fail}.
nounactionpatt(P) --> snoop(S0,S0),
                                        % SO is the input string
                    { \+ checkst(nounactionpatt,1,_,_,S0,_)},
                      actionlmod(L, Syn1),
                      nounactionunit(A),
                      actionrmod(R, Syn2),
```

```
snoop(S,S),
                     { (Syn1 = ved, append(R,[A], RA),
                       append(L, RA, P);
                        Syn1 = ving, append(R, [A], RA),
                       L = [action, Verb, Object],
                       modlist (RA, Object, Mods).,
                        frame(P, action, Verb, Mods)),
                        addst(nounactionpatt,1,s,P,S0,S) }.
% no more nounactionpatt - save failure
nounactionpatt(_) --> addst(nounactionpatt,0,f,_), {!, fail}.
% the central unit of the nounactionpatt is a nounactpatt or a process
nounactionunit(A) --> nounactpatt(A).
nounactionunit(A) --> process(A).
% left modifiers of nounactpatt
% Zvad-inhibited cleavage pf Ps1
actionlmod(L, ved) --> substances(S),
                      optdash,
                      action(Sem, [ved], Target, Features),
                     { frame(L, action, Target, [S]) }.
% apoptosis induced cleavage of ps2
actionlmod(L, ved) --> process(S),
                      optdash,
                      action(Sem, [ved], Target, Features ),
                     { frame(L, action, Target, [S]) }.
% apoptosis causing cleavage of Ps1 by Zvad.
% need to invert the order of nounactpatt and action1mod
actionlmod(L, ving) --> processobject(A), % process or nounacpatt,
                       action(Sem, [ving], Target, Features),
                      { frame(L,action, Target,A) }.
actionlmod([],_) --> [].
actionrmod(R,ved) --> action(Sem,[ved],Target,Features),
                      byagent(A), % may have to add ving to actionrmod
                    { frame (R, action, Sem, A) }.
actionrmod([],_) --> [].
% actpatt parses a simple action between substances expressed by an active verb
% actpatt is saved in a symbol table (st); check for success/failure % % 1st
% Case where actpatt is in st and has been successful
actpatt(F) --> checkst(actpatt,_,s,F).
% Case where actpatt is in st as a failure.
actpatt(_) --> checkst(actpatt,_,f,_), {!, fail}.
% actpatt 1: substance acts on substance
% PDK1 phosphorylates p70s6k at Thr229
actpatt(F) -->
    snoop(S0,S0), % S0 is the input string
  { \+ checkst(actpatt,1 ,_,_,S0,_)},
```



```
substances (A1),
    sem whichrel,
                      % opt 'that'
    action (Semclass, [vp, ved], Target, Features),
    prepopt, % added prepopt to allow action 'to' and 'with' substance
    substances (A2),
    siteinfo(Site),
    snoop(S,S),
  { (member(def, Features),
    modlist([A1, A2, Site], Mods);
    member (rev, Features),
    modlist([A2,A1,Site],Mods)),
    frame (F, action, Target, Mods),
    addst(actpatt,1,s,F,S0,S)
  }.
% acpatt 2:
% Substance was bound by Substance
% Substance was associated to substance.
% F can give either first or second place to the second argument;
% a byagent gets first position; prepagent gets second.
Phosphorylated Fyn was associated with Cbl.
actpatt(F) -->
    snoop(S0,S0), % S0 is the input string
 { \+ checkst(actpatt, 2, _, _, S0, _) }.
    substances (A1),
    sem beterm(),
    action (Semclass, [ven], Target, Features),
    optbyorprepagent (Position, A2),
    snoop(S,S),
 { (member(def, Features),
   (Position=second, modlist([A1,A2,Site],Mods);
    Position = first, modlist([A2,A1,Site],Mods));
    member (rev, Features),
   (Position=second, modlist([A2,A1,Site],Mods);
    Position= first, modlist([A1,A2,Site],Mods))),
    frame (F, action, Target, Mods),
    addst(actpatt, 2, s, F, S0, S)
 }.
% no more actpatt - save failure
actpatt() --> addst(actpatt,0,f,_), {!, fail}.
% nounactpatt parses a simple action between substances expressed by a nominal
% verb
% nounactpatt is saved in a symbol table (st); check for success/failure 1st
% Case where nounactpatt is in st and have been successful
nounactpatt(Fmt) --> checkst(nounactpatt, ,s,Fmt).
% Case where nounactpatt is in st as a failure.
nounactpatt(_) --> checkst(nounactpatt,_,f,_), {!, fail}.
% nounactpatt 1:
% Jnk phosphorylation of Bad
nounactpatt(F) -->
    snoop(S0,S0), % S0 is the input string
```

```
{ \+ checkst(nounactpatt, 1, _, _, 50, _) },
    substances(A1),
    {aminoacidtest(A1)},
    optdash,
    action (Semclass, [n], Target, Features),
    ofobject (A2),
    siteinfo(Site),
    snoop(S,S),
   { (member(def, Features),
     modlist([A1,A2,Site],Mods);
     member (rev, Features),
     modlist([A2,A1,Site],Mods)),
     frame (F, action, Target, Mods),
     addst (nounactpatt, 1, s, F, S0, S)
   }.
% nounactpatt 2: the binding of substance and substance
% association of Fyn and Cbl.
% the reason for having this as a separate pattern is to
% prevent 'Fyn and Cbl' from being parsed together as substances
nounactpatt(F) -->
    snoop(S0,S0), % S0 is the input string
 { \+ checkst(nounactpatt, 2 , _ , _ , S0, _) },
    action(attach, [ving, n], Target, Features),
    ofobject1(A1),
    andobject (A2),
 siteinfo(Site),
    snoop(S,S),
 { modlist([A1,A2,Site],Mods),
    frame (F, action, Target, Mods),
    addst(nounactpatt, 2, s, F, S0, S)
* nounactpatt 3:
* The cleavage of protein by substance.
* Association of phosphorylated Fyn with Cbl
* Tyrosine phosphorylation of Cbl by kinase
t optbyorprepagent determines the order of arguments; byagent is placed first;
* prepagent is placed second
nounactpatt(F) -->
   snoop(S0,S0), % S0 is the input string
    { \+ checkst(nounactpatt, 3 , _, _, S0, _) },
    actionof(F),
    snoop(S,S),
  { addst(nounactpatt, 3 , s, F, S0, S) }.
actionof(F) -->
    siteinfo(Site).
    action(Semclass, [ving, n], Target, Features),
    optofobject (A1),
    optbyorprepagent (Position, A2),
    snoop(S,S),
  { (member(def, Features),
     (Position=second, modlist([A1,A2,Site],Mods);
     Position= first, modlist([A2,A1,Site],Mods));
     member (rev, Features),
```

```
(Position=second, modlist([A2,A1,Site],Mods);
     Position= first, modlist([Al,A2,Site],Mods))),
     frame (F, action, Target, Mods)
  }.
% nounactpatt 4:
% Fyn association with Cbl.
nounactpatt(F) -->
    snoop(S0,S0), % S0 is the input string
  { \+ checkst(nounactpatt, 4, _, _, S0, _) },
    substances (A1),
    action(Semclass,[ving,n], Target, Features),
    withobject (A2),
  % siteinfo(Site),
    snoop(S,S),
 { modlist((A1, A2, Site), Mods),
    frame (F, action, Target, Mods),
    addst(nounactpatt, 4, s, F, S0, S)
 }.
aminoacidtest(X) :- X \= [aminoacid ].
% nounactpatt 5:
% IL-2 gene transcription
% Cbl phosphorylation [by substance or action]
nounactpatt(F) -->
    snoop(S0,S0), % S0 is the input string
    \+ checkst(nounactpatt,5 ,_,_,S0,_) },
    substances (A2),
    optdash,
    action (Semclass, [n], Target, Features),
    optbyagent (A1),
 % siteinfo(Site),
    snoop(S,S),
 { (member(def, Features),
    modlist([A1, A2, Site], Mods);
    member (rev. Features),
    modlist([A2,A1,Site],Mods)),
    frame (F, action, Target, Mods),
    addst(nounactpatt, 5 ,s,F,S0,S)
 }.
% nounactpatt 6:
% fyn-cbl association.
nounactpatt(F) -->
    snoop(S0,S0), % S0 is the input string
    \+ checkst(nounactpatt,6 ,_,_,S0,_) },
   'substances(Al),
    optdash,
    substances (A2),
    action(Semclass, [n, ving], Target, Features),
 % siteinfo(Site),
    snoop(S,S),
  { modlist([A1,A2,Site],Mods),
    frame (F, action, Target, Mods),
    addst (nounactpatt, 6, s, F, S0, S)
  }.
```

```
% nounactpatt 7:
% Cbl phosphorylated by fyn.
nounactpatt(F) -->
    snoop(S0,S0), % S0 is the input string
    { \+ checkst(nounactpatt,7 ,_,_,S0,_)},
    substances (A1),
    action(Semclass, [ven], Target, Features).
    [by],
    substances (A2),
 $ siteinfo(Site),
    snoop(S,S),
             { (member(def, Features),
    { modlist([A2,A1,Site],Mods),
             member (rev, Features),
 ¥.
             modlist([A1, A2, Site], Mods)),
      frame (F, action, Target, Mods),
      addst(nounactpatt,7,s,F,S0,S)
    }.
% no more nounactpatt - save failure
nounactpatt(_) --> addst(nounactpatt,0,f,_), {!, fail}.
connectact (Sem, Syn, Target, Features) -->
      action(Sem, Syn, Target, Features),
     {member(Sem, [cause, cause1, activate, inactivate, signal, substitute, promote])}.
connectacts (Sem, Syn, Target, Features) -->
      connectact (Sem, Syn, Target, Features).
% aminoacid like tyrosine : ex.: tyrosine Cbl phosphorylation
% at position 201 Thr
siteinfo(S) --> aminoacid(A),
                  {frame(S, site, [A], [])} .
siteinfo(S)
                 sitepreps, % 'in', 'at'
                 position(S).
siteinfo([]) --> [].
              --> prepterm(in,_).
sitepreps
              --> prepterm(at,_).
sitepreps
position(S)
             --> [position],
                  sem integerterm(I),
                { frame(S, site, I, []) }.
* The definitions of actions refer to the lexicons lexsynact.pl and lexsemact.pl
% Sem is the semantic class; Syn is the syntactic class
% F is the target
% oneaction was added for use with moreaction to allow parsing of conjoined
% actions
oneaction(activate, Syn, F, Features)
                                        --> activateterm(Syn, F, Features), {!}.
oneaction(attach, Syn, F, Features)
                                        --> attachterm(Syn,F,Features),{!}.
oneaction (breakbond, Syn, F, Features)
                                       --> breakbondterm(Syn,F,Features), {!}.
```

```
--> createbondterm(Syn, F, Features), {!}.
oneaction(createbond, Syn, F, Features)
                                         --> inactivateterm(Syn, F, Features), {!}.
oneaction(inactivate, Syn, F, Features)
oneaction(react, Syn, F, Features)
                                         --> reactterm(Syn, F, Features), {!}.
oneaction(release, Syn, F. Features)
                                          --> releaseterm(Syn, F, Features), {!}.
oneaction(signal, Syn, F, Features)
                                          --> signalterm(Syn, F, Features), {!}.
                                         --> substituteterm(Syn, F, Features), {!}.
oneaction(substitute, Syn, F, Features)
                                         --> transcribeterm(Syn, F, Features), (!).
oneaction(transcribe, Syn, F, Features)
                                         --> promoteterm(Syn, F, Features), (!).
oneaction(promote, Syn, F, Features)
                                         --> generateterm(Syn, F, Features), {!}.
oneaction (generate, Syn, F, Features)
oneaction(cause, Syn, F, Features)
                                             causeterm(Syn, F, Features), {!}.
action(activate, Syn, F, Features)
                                      --> activateterm(Syn, A1, Features),
                             moreaction(Conj, Args),
                            \{Conj = [], F = A1;
                            Conj\=[], mergemods([[action,Al]],Args,Actions),
                            frame(F1, relation, Conj, Actions), F = [F1] }.
                                      --> attachterm(Syn, A1 , Features),
action(attach, Syn, F, Features)
                            moreaction (Conj, Args),
                            {Conj = [], F = A1;}
                            Conj\=[], mergemods([[action,A1]],Args,Actions),
                            frame(F1, relation, Conj, Actions), F = [F1]).
                                     --> breakbondterm(Syn, F, Features),
action(breakbond, Syn, F, Features)
                            moreaction(Conj,Args),
                            \{Conj = [], F = A1;
                            Conj\=[], mergemods([[action, Al]], Args, Actions),
                            frame (F1, relation, Conj, Actions), F = [F1] }.
action(createbond, Syn, F, Features) --> createbondterm(Syn, F, Features),
                            moreaction(Conj, Args),
                            {Conj = [], F = A1;}
                            Conj\=[], mergemods([[action,A1]],Args,Actions),
                            frame (F1, relation, Conj, Actions), F = [F1] }.
action(inactivate, Syn, F, Features) --> inactivateterm(Syn, F, Features),
                            moreaction(Conj, Args),
                            {Conj = [], F =A1;
                            Conj = [], mergemods ([[action, A1]], Args, Actions),
                            frame (F1, relation, Conj, Actions), F = [F1] }.
action(react, Syn, F, Features)
                                      --> reactterm(Syn, F, Features),
                            moreaction (Conj, Args),
                            {Conj = [],F =A1;
                            Conj = [], mergemods ([[action, Al]], Args, Actions),
                            frame(F1, relation, Conj, Actions), F = [F1]}.
                                      --> releaseterm(Syn,F,Features),
action(release, Syn, F, Features)
                            moreaction(Conj, Args),
                            {Conj = {}, F = A1;}
                            Conj = []; mergemods ([[action, Al]], Args, Actions),
                            frame (Fl. relation, Conj. Actions), F = [F1] }.
action(signal, Syn, F, Features)
                                     --- signalterm(Syn, F, Features),
                            moreaction(Conj, Args),
                            \{Conj = [], F \approx A1;
                            Conj\=[], mergemods([[action,A1]],Args,Actions),
                            frame(F1, relation, Conj, Actions), F = [F1]}.
action(substitute,Syn,F,Features) --> substituteterm(Syn,F,Features),
                            moreaction (Conj, Args),
                            \{Conj = [], F = A1;
                            Conj = [], mergemods ([[action, A1]], Args, Actions),
                            frame (F1, relation, Conj, Actions), F = [F1] }.
action(transcribe, Syn, F, Features) --> transcribeterm(Syn, F, Features),
```

```
moreaction(Conj, Args),
                            {Conj = [},F =A1;
                            Conj\=[], mergemods([[action, Al]], Args, Actions),
                            frame (F1, relation, Conj, Actions), F = [F1] }.
action(promote, Syn, F, Features)
                                      --> promoteterm(Syn, F, Features),
                            moreaction(Conj, Args),
                            {Conj = [], F = A1;}
                            Conj\=[], mergemods([[action, Al]], Args, Actions),
                            frame (F1, relation, Conj, Actions), F = [F1] }.
action(generate,Syn,F,Features)
                                     --> generateterm(Syn, F, Features),
                            moreaction(Conj, Args),
                            {Conj = [], F = A1;}
                            Conj\=[], mergemods([[action, A1]], Args, Actions),
                            frame(F1, relation, Conj, Actions), F = [F1] }.
action(cause, Syn, F, Features)
                                  --> causeterm(Syn, F, Features),
                            moreaction(Conj, Args),
                            {Conj = [],F =A1;
                            Conj\=[], mergemods([[action,A1]],Args,Actions),
                            frame (F1, relation, Conj, Actions), F = [F1] }.
% binds, phosphorylates and activates
moreaction(Conj, Args) --> sem conjrest(Conjl),
                            oneaction (Sem, Syn, A, Features),
                            moreaction(Conj2, Alist),
                           {Conj2 = [], Alist=[], Conj=Conj1, Args = [[action, A]];
                            Conj2 = [], Conj = Conj2,
                            addmod([action, A], Alist, Args) }.
moreaction([],[],S,S).
passiveconnect(Sem, [ven], Target, Features) -->
                  sem_beterm(_),
                  connectact (Sem, [ven], Target, Features).
processpatt(A) --> disease(A).
processpatt(A) --> process(A).
optbyorprepagent(first,A) --> byagent(A).
optbyorprepagent(second, A) --> prepagent(A).
optbyorprepagent(first,A) \longrightarrow [], \{A = x\}.
byorprepagent(first,A) --> byagent(A).
byorprepagent (second, A) --> prepagent (A).
optbyagent(A) --> byagent(A).
optbyagent(A) --> [], \{A = [x]\}.
byagent(A) --> [by],
               substances (A).
byagent(A) --> [by],
                nounactionpatt(A).
prepagent(A) --> withobject(A).
prepagent(A) --> toobject(A).
% prepagent(A) --> andobject(A).
prepagent(A) --> ofobject(A).
```

```
% optprepagent(A) --> byagent(A).
optprepagent (A) --> ofobject (A).
optprepagent(A) --> withobject(A).
optprepagent(A) --> toobject(A).
optprepagent(A) --> andobject(A).
optprepagent(A) --> [], {A= [x]}.
ofobject(A) --> [of],
                nounactionpatt(A).
ofobject(A) --> [of],
                substances(A).
ofobject(A) --> [of],
                actionof(A).
ofobject1(A) --> [of], substance(A). * to parse Binding of Fyn and Bad.
optofobject(A) --> ofobject(A).
optofobject([x]).--> [].
processobject(A) --> process(A). * can be expanded to nounactpatt, etc.
% optwithobject(A) --> withobject(A).
* optwithobject(A) --> [], \{A = \{x\}\}.
withobject(A) --> [with], substances(A).
toobject(A) --> [to], substances(A).
andobject(A) --> [and], substances(A).
prepobject(A) --> [to], substances(A).
prepobject(A) --> [with], substances(A).
optbyarg(A) --> [by],
             actionarg(A).
optbyarg(A) --> substances(A).
optbyarg(A) --> [], {A = ['substance unknown']}.
prepopt --> [to].
prepopt --> [with].
prepopt --> [by].
prepopt --> [of].
prepopt --> [].
% toopt
toopt --> [to].
toopt --> [].
% withopt
withopt --> [with].
withopt --> [].
            --> ['-'].
optdash
            -->[].
optdash
optof
optof
            --> [of].
/* optactionarg(A) --> actionarg(A).
optactionarg([]) --> []. */
optactionarg(A) -->
      actionarg(A).
```

```
there is no further argument
optactionarg(A) -->
    [],
    {A = {I}}.
% substances(F) --> substance(F).
% substances(F) --> substance(P1),
              moresubstances(Conj, Plist),
               { Conj = [], Plist = [], F = Pl ;
용
욯 .
               Conj \= [],
¥
             mergemods (P1, Plist, Args),
                 frame (F, relation, Conj, Args)
$ substances(F) --> substanceswithmods(F).
% substances(A) -->
                  proteins (A).
% subswithmods.txt
% substances is saved in a symbol table (st);
% check for success/failure 1st
* Case where substances is in st and has been successful
substances(Fmt) --> checkst(substances, ,s,Fmt).
% Case where substance is in st as a failure.
substances(_) --> checkst(substances,_,f,_), {!, fail}.
substances(F) -->
        snoop(S0,S0),
      { \+ checkst(substances,1,s,_,S0,_)},
        lmods(Lmods), % left modifiers
        (severalsubstances([relation,Conj,First|Rest]), & conjoined substances
        rmods (Rmods),
                         % right modifiers
% create list of lists containing distributed mods. of substances
      { distributesubs(Dist,[First|Rest],Lmods,Rmods),
% check Lmods - "no" F1 or F2 should be changed to no F1 and no F2
        fixconj(Lmods,[rel,Conj],[rel,C2]),
       %splice([Conj,Dist],F)
        frame (F, relation, C2, Dist) };
* substances and modifiers without conjunction
        substance (D1),
        rmods (Rmods),
        {D1 = [Type1, Substance1 | ModsD1],
        delete(ModsD1, [], ModsD2),
        append([Lmods, Rmods], ModsD2, Allmods1),
        delete(Allmods1, [], Allmods2),
        frame(F, Type1, Substance1, Allmods2) }) ,
        snoop(S,S),
       {addst(substances,1,s,F,S0,S)}.
/* substances(F) --> snoop(S0,S0),
                  {\+ checkst(substances, 3 , s, _, S0, _)},
                  complex(F),
                  {addst(substances, 3, s, F, S0, S)}.
% no more substances- save failure
substances(_) --> addst(substances,0,f,_), {!, fail}.
```

```
severalsubstances(F) --> substance(P1),
                         moresubstances (Conj, Plist),
                      { Conj = [], Plist = [], F = P1;
                         Conj \= [],
                         addmod(Pl,Plist,Args),
                         frame (F, relation, Conj, Args)
% ' X, Y, and Z'
moresubstances(Conj, Args) --> sem conjrest(Conj1),
                           substance (P1),
                           moresubstances(Conj2, Plist),
                        { Conj2 = [], Plist = [], Conj = Conj1, Args = [P1];
                           Conj2 = [], Conj2 = /, Conj = Conj2,
                           addmod(P1,Plist,Args)
% to allow for substances with modifiers
moresubstances(Conjl, Args) --> sem_conjrest(Conjl),
                               substances (Args), {!}.
moresubstances([],[]) --> []. % no conjunction
% distributesubs
% distributes left mods and right mods over list of findings creating
% list of lists of findings with mods
distributesubs([],[],_,_) :- !.
distributesubs (Dist, [D1 | Tail], Lmods, Rmods) :-
        distributesubs(Dist2, Tail, Lmods, Rmods), %distributed for remainder
        D1 = [Type1, Substance1 [ModsD1],
        append([Lmods, Rmods], ModsD1, Allmods1),
        delete(Allmods1,[],Allmods2),
        frame (D, Type1, Substance1, Allmods2),
       append([D], Dist2, Dist). % Combine findings to get list of findings
lmods(A) --> stateterm(F),
           {frame(A, state, F, [])}.
lmods([]) --> sem_measure(_).
lmods([]) --> [].
rmods([]) --> [].
stateterm(F) --> acclex(state, F).
% for past participle of createbond and breakbond actions, the target
* is the word. ex.: phosphorylated, dephosphorylated, methylated
stateterm(F) -->
            snoop(S0,S0), % get the initial string
            createbondterm([ven], _,_),
            {SO = [F|]}. %get the first word of the string
stateterm(F) -->
            snoop(S0,S0), % get the initial string
            breakbondterm([ven], _,_),
            {SO = [F] }}. %get the first word of the string
% may have to add attachterm for 'bound'
```

```
% Taken from MedLEE grammar to handle '3 cm'
sem measure(M) -->
                   sem premeasure,
                   sem_quantityterm(N),
                   optdash,
                   sem_measureterm(Unit),
                 { frame(M, measure, [N, Unit], []) }.
% complex predicates added November 8, 1999
% CrkL-C3G complex
% ras: raf-1 association
% ras: raf-l complexes
% shc-grb2-sos
% TCR/CD3 complex
% p/CAF-p/CIP-CBP/p300-SRC-1 complex
% Ras:Raf-1 complexes
complex(C) -->
                 proteins(P),
                  {P = [A,B]_A = [], B = []},
                   optcomplexword,
                 { frame(C, complex, [P], []) }.
% a complex of NFAT4 with calcineurin
complex(C)
                 complexword,
            -->
                   complexarg(A),
                   {frame(C, complex, [A], []) }.
complexarg(A) --> [of], proteins(A).
complexarg(A) --> [between], proteins(A).
% a complex between MyD88, IRAK-2, and the IL-1Rs
complexarg(A) --> action(contain), proteins(A).
% Complexes containing BOB.1/OBF.1 and Oct proteins
            --> protein(A),
proteins(P)
                 moreproteins (P1),
                 {(A\=[]; append([A],P1,P))}.
moreproteins(A) --> proteinconnector,
                    proteins (A).
moreproteins([]) --> [].
proteinconnector --> ['-'].
                      ['/'].
proteinconnector -->
proteinconnector -->
                       [':'].
% connector -->
                  [','].
                            taken out not to conflict with relation in
                                                               moresubstances
% connector -->
                    [and].
proteinconnector(C) --> [with].
                    proteinconnector.
optconnector -->
optconnector -->
                    [].
complexword --> [complex].
complexword --> [complexes].
complexword --> ['signaling complexes'].
optcomplexword
                   --> complexword.
optcomplexword
                   --> [].
substance(A) --> protein(A).
```

```
substance(A) --> cell(A).
substance(A) --> species(A).
substance(A) --> structure(A).
substance(A) --> domain(A).
substance(A) --> gene(A).
substance(A) --> geneorprotein(A).
substance(A) --> aminoacid(A).
substance(A) --> smallmolecule(A).
substance(A) --> matter(A).
substance(A) --> proteinsite(A).
substance(A) --> disease(A).
                                        % this will be modified later
substance(A) --> complex(A).
protein(A) -->
    proteinterm(P),
    {frame(A, protein, P, [])}.
complex(A) -->
    complexterm(P),
    {frame(A, complex, P, [])}.
cell(A) -->
    cellterm(P),
    {frame(A, cell, P, [])}.
species(A) -->
    speciesterm (P),
    {frame(A, species, P, [])}.
structure(A) -->
    structureterm(P),
    \{frame(A, structure, P, [])\}.
domain(A) -->
    domainterm(P),
    {frame(A; domain, P, [])}.
gene(A) -->
    geneterm(P),
    {frame(A,gene,P,[])}.
geneorprotein(A) -->
    gpterm(P),
    (X),
    \{(X = gene, frame(A, gene, P, []);
      X = protein, frame(A, protein, P, []);
      X = gene, X \= protein, frame(A, geneorprotein, P, ())).
aminoacid(A) -->
    aminoacidterm(P),
    {frame(A, aminoacid, P, [])}.
smallmolecule(A) -->
    smallmoleculeterm(P),
    {frame(A,'small molecule',P,[])}.
matter(A) -->
```

```
matterterm(P),
    {frame(A, substance, P, [])}.
proteinsite(A) -->
    proteinsiteterm(P),
    {frame(A, 'protein site', P, {})}.
disease(A) -->
    diseaseterm(P),
    {frame(A, disease, P, [])}.
process(A) -->
     processterm(Syn, F, Features),
     {frame(A, process, F,[]),!}.
process(A) -->
     processterm(P),
     {frame(A, process, P, {}),!}.
% terminals
proteinterm(F)
                      --> acclex(protein, F).
complexterm(F)
                     --> acclex(complex,F).
cellterm(F)
                      --> acclex(cell,F).
speciesterm(F)
                      --> acclex(species,F).
structureterm(F)
                     --> acclex(structure, F).
domainterm(F)
                      --> acclex(domain,F).
                      --> acclex(gene,F).
geneterm(F)
                      --> acclex(gp,F).
gpterm(F)
aminoacidterm(F)
                     --> acclex(aminoacid,F).
smallmoleculeterm(F) --> acclex(smallmolecule,F).
matterterm(F)
                      --> acclex(substance, F).
proteinsiteterm(F)
                     --> acclex(proteinsite,F).
                      --> acclex(disease,F).
diseaseterm(F)
processterm(F)
                      --> acclex(process, F).
% action(activate,Syn,F,Features) --> activateterm(Syn,F,Features).
activateterm(Syn,F,Features) --> acclexss(activate, Syn,F,Features).
attachterm(Syn, F, Features) --> acclexss(attach, Syn, F, Features).
breakbondterm(Syn, F, Features) --> acclexss(breakbond, Syn, F, Features).
createbondterm(Syn,F,Features) --> acclexss(createbond, Syn,F,Features).
inactivateterm(Syn,F,Features) --> acclexss(inactivate, Syn,F,Features).
                             --> acclexss(react, Syn,F,Features).
reactterm(Syn.F.Features)
releaseterm(Syn,F,Features) --> acclexss(release, Syn,F,Features).
signalterm(Syn, F, Features)
                              --> acclexss(signal, Syn, F, Features).
substituteterm(Syn,F,Features) --> acclexss(substitute, Syn,F,Features).
transcribeterm(Syn, F, Features) --> acclexss(transcribe, Syn, F, Features).
promoteterm(Syn, F, Features)
                            --> acclexss(promote, Syn, P, Features).
                              --> acclexss (process, Syn, F, Features).
processterm(Syn, F, Features)
generateterm(Syn,F,Features) --> acclexss(generate,Syn,F,Features).
                              --> acclexss (cause, Syn, F, Features).
causeterm(Syn,F,Features)
% Semlist contains a phrase which is an action
actionchk(Semlist) :-
       intersect (Semlist, [attach, cause, createbond, breakbond, activate,
                 inactivate, substitute, transcribe, express, promote, signal).
% Semlist contains a phrase which is a connector action
```

18

intersect (Semlist, [cause, activate, inactivate, substitute,

connectchk(Semlist) :- '

```
promote, signal]).
Genome sectionc: ends here
% relations are connected by conjunctions, or
          certain 'conn' prepositions.
* Taken from MedLEE grammar to handle connectives that are conjunctions
         Ex: "severe markings, possibly from tuberculosis"
sem relation(F, []) -->
                       % relation and modifiers
       sem commapunc,
       sem_certainty([],C,rel),
       prepterm (P, conn),
       {frame(F, rel, P, C)}.
       %plice([[rel,P],C],R).
           Ex: "markings, swelling", "markings and swelling"
sem_relation(R,[]) --> sem_conjrel(R),
                     sem_commapunc.
          "density may represent known tumor"
    "markings, and swelling"
sem conjrel(F) -->
      sem commapunc,
      sem conjterm(Conj),
      {frame(F, rel, Conj, [])}.
sem conjrest(Conj) -->
                        % restricted conj, has not sem relation showopt
       sem commapunc,
       sem conjterm(Conj).
"markings, swelling"
sem_conjrest(',') -->
     snoop($0,50),
       sem commapunc,
     snoop(S,S),
      {SO } = S.
* Treatment of Verbs from MedLEE's Grammar
            form of "be"
sem_auxverb(B) --> sem_beterm(B).
            form of "do"
sem_auxverb(B) --> sem_doterm(B).
            form of "have"
.
sem auxverb(B) --> sem haveterm(B).
sem_recrel --> prepterm(in,_).
sem_recrel --> prepterm(to,_).
% "is not"
sem_auxrel(V) --> sem_auxverb(),
                sem_negterm(V).
sem_auxrel(V) --> sem_auxverb(V).
* left modifiers of findings include negation, quantity, certainty, degree, and
```

change type modifiers

```
sem_integer(W) --> [W], {integer(W)}.
sem integer(W) --> integerterm(W).
sem timeunit(T) --> sem timeunitterm(T).
% From MedLEE grammar - "lasting 2 days", "for 2 days", "times 2 days"
sem_duration(F) -->
       sem durpreps,
       sem premeasure, %about
       sem_timemeasure(T),
       sem_durationmod, % opt. - "in duration"
       {frame(F, duration, [T], [])}.
sem_duration([],S,S).
sem_durpreps -->[times].
sem_durpreps -->
    prepterm(for,_).
sem_durpreps -->[lasting,for].
sem_durpreps -->[lasting].
sem_durpreps -->[lasted, for].
sem_durpreps -->[lasted].
sem_durationmod -->
         sem aposts, %opt. - "'s"
        [duration].
sem_durationmod --> [in], [duration].
sem_durationmod --> [].
sem_aposts --> [''''], [s].
sem_apost --> [].
% sem_frequency taken From MedLEE's grammar
% "two times", "times two", "two times a/per week", "two times daily"
sem frequency(F) -->
        sem_freqterm(F1),
                             % "once"
                           % "a day"
        sem freqterm(F2),
        {frame(M, unitval, [F1, F2], []),
         frame(F, frequency, [M], [])}.
sem frequency(F) -->
        sem_freqterm(M), % "qid", "daily"
        {frame(F, frequency, M, [])}.
% "2 times",
sem frequency(F) -->
        sem premeasure,
        sem_quantityterm(M),
        sem times,
      {frame(F, frequency, [M], [])}.
% "times 2"
sem_frequency(Q) -->
        sem times,
        sem_quantityterm(Q1),
        {frame(Q, frequency, Q1, [])}.
sem frequency(F) -->
        [q], sem_quantityterm(Q),
             sem_timeunit(T),
        {frame(F, frequency, [unitval, [Q,T]], [])}.
```

```
sem frequency(F) --> sem_eachevery,
                       sem quantityterm(Q),
                       sem timeunit(T),
                     {frame(F, frequency, [unitval, [Q, T, every]], [])}.
sem frequency(Q) -->
                         % "second"
         sem ordinal (O),
         sem_timeopt,
         {frame(Q, frequency, O, [])}.
sem_frequency([],S,S).
sem_timeopt --> [time].
sem_timeopt --> [].
sem_eachevery --> [each].
sem_eachevery --> [every].
sem times --> [times].
sem times -->[x].
% Taken from MedLEE's grammar
negation modifier - "no" as in "no cardiomegaly"
sem negation(F) -->
        sem negterm(N),
         {frame(F,neg,N,[])}.
% negation not present
sem_negation([],S0,S0).
% Taken from MedLEE's grammar
% quantity modifier - "two" as in "two masses"
sem_quantity(F) -->
       snoop (S0, S0),
        { \+ checkst(sem_dates, 1, s, _, SO, _) }, % not a legitimate date
       sem_quantityterm(Q),
       sem_quantityrmod(_),
                                    % "2 or 3", "2 to 3"
                                    % rule out '2 mm'
        { \+ next_wordunit($0),
        frame (F, quantity, Q, [])
        }.
sem_quantity([],S0,S0).
sem commapunc([','[S],S).
sem commapunc(S,S).
sem_conjterm(C)
                     --> acclex(conj,C).
sem_doterm(D)
                     --> acclex(vdo,D).
sem_endmark([.|S],S).
sem endmark([;|S],S).
sem_freqterm(F)
                     --> acclex(freq,F).
sem_haveterm(H)
                     --> acclex(vhave, H).
integerterm(I)
                     --> acclex(integer, I).
sem_measureterm(M) --> acclex(unit,M).
                     --> acclex(med,M).
sem medterm(M)
sem negterm(N)
                     --> acclex(neg,N).
prepterm(P,C)
                     --> acclex(p, [P,C]).
sem timeunitterm(T) --> acclex(timeunit,T).
```

```
% lexog - adapted from MedLEE lexicon
88888888888888888888
                      NEGATIONS
                                :-unknown(_,fail).
:-multifile(wdef/3).
wdef(cannot, neg, no).
wdef (neither, neg, no).
wdef (never, neg, no).
wdef (no, neg, no).
wdef (non, neg, no).
wdef (none, neg, no).
wdef (not, neg, no).
wdef (nothing, neg, no).
************
                      wdef('&',conj,and).
wdef('/',conj,or).
wdef('-',grammar,'-').
wdef('+',conj,and).
wdef(although,conj,and).
wdef (and, conj, and).
wdef(as,conj,and).
wdef (because, conj, and).
wdef (but, conj, and).
wdef(',',conj,',').
wdef(except,conj,no).
%wdef(if,grammar,if).
wdef(minus,conj,no).
wdef(nor,conj,no).
wdef(or,conj,or).
wdef(that, grammar, that).
wdef (though, conj, and).
wdef (thru, conj, and).
wdef (verses, conj, or).
wdef (versus, conj, or).
wdef (vs, conj, or).
wdef (when, grammar, when).
wdef (where, grammar, where).
wdef (whereas, conj, and).
wdef (which, grammar, which).
wdef (while, conj, and).
wdef (who, grammar, who).
wdef (yet, conj, and).
$$$$$$$$$$$$$$$$$$$$$$$$$ PREPOSITIONS $$$$$$$$$$$$$$$$$$$$$$$$
wdef(above,ploc,above).
wdef(about,p,[approximately,nconn]).
wdef(about,ploc,about).
wdef (across, ploc, across).
wdef(abutting,ploc,near).
wdef(accompanies,p,[with,conn]).
wdef(accompanying,p,[with,conn]).
wdef(adjacent,ploc,adjacent).
wdef(adjacent, region, adjacent).
wdef(after,p,[after,conn]).
wdef (after, tprep, after).
wdef(along,p, [on,nconn]).
wdef(approximately,p,[approximately,nconn]).
wdef(around,p,[approximately,nconn]).
```

```
wdef(at,p,[at,nconn]). .
wdef(atop,p,[on,nconn]).
wdef (before, ploc, before).
wdef (before, tprep, before).
wdef (behind, ploc, behind).
wdef (below, ploc, below) .
wdef (between, ploc, between).
wdef (beyond, ploc, beyond).
wdef(by,ploc,near).
wdef(despite,p,[with,conn]).
wdef (during, p, [during, conn]).
wdef (during, tprep, during).
wdef (encasing, ploc, encasing).
wdef(extending,p,[in,nconn]).
wdef(following,p,[after,conn]).
wdef(following,tprep,after).
wdef(for,p,[for,nconn]).
wdef(from,p,[from,conn]).
wdef(in,p,[in,nconn]).
wdef(including,p,[with,conn]).
wdef(into,p,[in,nconn]).
wdef(involving,p,[of,nconn]).
wdef(next,tprep,next).
wdef(occupying,p,[in,nconn]).
wdef(on,p,[on,nconn]).
wdef(of,p,[of,nconn]).
wdef (over, ploc, over).
wdef(overlie,ploc,over).
wdef (overlied, ploc, over).
wdef(overlies,ploc,over).
wdef(overlying,ploc,over).
wdef (prior, tprep, before).
wdef(near,ploc,near).
wdef (radiating, ploc, radiating).
wdef(regarding,p,[about,nconn]).
                                   % 'roughly 6 mm'
wdef (roughly, grammar, roughly).
wdef(since,p,[since,conn]).
wdef(since, status, subsequent).
wdef(through,p,[in,nconn]).
wdef(throughout,p,[in,nconn]).
wdef(to,p,[to,nconn]).
wdef(toward,p,[to,nconn]).
wdef(towards,p,[during.conn]).
wdef (under, ploc, below) .
wdef (underneath, ploc, below).
wdef(until,tprep,until).
wdef(up, grammar, up).
wdef(upon,p,[on,nconn]).
wdef(via,p,[with,conn]).
wdef(with,p,[with,conn]).
wdef(within,p,[in,conn]).
wdef(without,p,[no,conn]).
%wdef(without, neg, no).
wdef('%',unit,percent).
```

```
wdef(cc,unit,cc).
wdef(centimeter, unit, cm).
wdef(centimeters, unit, cm).
wdef(cm, unit, cm).
wdef (degrees, unit, degree).
wdef(gm,unit,gram).
wdef (gms, unit, gram).
wdef (gram, unit, gram).
wdef (grams, unit, gram).
wdef(kg,unit,kilogram).
wdef(kilo,unit,kilogram).
wdef(kilogram, unit, kilogram).
wdef(kilograms, unit, kilograms).
wdef(liter, unit, liter).
wdef(liters,unit,liter).
wdef (microgram, unit, microgram).
wdef (micrograms, unit, microgram).
wdef(milliliter,unit,ml).
wdef(milliliters, unit, ml).
wdef(milligram, unit, mg).
wdef(milligrams,unit,mg).
wdef(milliseconds,unit,millisecond).
wdef(millivolts,unit,millivolt).
wdef(ml,unit,ml).
wdef(millimeter,unit,mm).
wdef (millimeters, unit, mm).
wdef(mm, unit, mm).
wdef(ozs,unit,ounce).
wdef (percent, unit, percent).
*$$$$$$$$$$$$$$$$$$$$$$$$$$$$$ NUMBERS $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
wdef(half,integer,'one half').
wdef (semi, quantity, semi).
wdef(ii,integer,2).
wdef(iii, integer, 3).
wdef(vi,integer,4).
wdef(v,integer,5).
wdef(vi,integer,6).
wdef(vii,integer,7).
wdef(viii,integer.8).
wdef(ix,integer,9).
wdef(xii,integer,12).
wdef(xiii,integer,13).
wdef (one, integer, 1).
wdef(two,integer,2).
wdef (double, quantity, double).
wdef(three,integer,3).
wdef (four, integer, 4).
wdef (quadruple, quantity, quadruple).
wdef(five,integer,5).
wdef(six,integer,6).
wdef(sixty,integer,60).
wdef (seven, integer, 7).
wdef (eight, integer, 8).
wdef(nine,integer,9).
wdef(ten,integer,10).
wdef(eleven,integer,11).
wdef(twelve,integer,12).
```

```
wdef (thirteen, integer, 13).
wdef (fourteen, integer, 14).
wdef (fifteen, integer, 15).
wdef (sixteen, integer, 16).
wdef (seventeen, integer, 17).
wdef (eighteen, integer, 18).
wdef (nineteen, integer, 19).
wdef (twenty, integer, 20).
wdef (thirty, integer, 30).
wdef(forty,integer,40).
wdef(fifty,integer,50).
wdef(sixty,integer,60).
wdef (seventy, integer, 70).
wdef(eighty,integer,80).
wdef (ninety, integer, 90).
wdef (hundred, integer, 100).
wdef (thousand, integer, 1000).
wdef(million,integer,1000000).
wdef(billion,integer,billion).
wdef(zero,integer,0).
wdef(first,ointeger,1).
wdef(second,ointeger,2).
wdef(third,ointeger,3).
wdef (fourth, ointeger, 4).
wdef(fifth,ointeger,5).
wdef (sixth, ointeger, 6).
wdef (seventh, ointeger, 7).
wdef (eighth, ointeger, 8).
wdef (ninth, ointeger, 9).
wdef (tenth, ointeger, 10).
wdef (eleventh, ointeger, 11).
wdef (twelvth, ointeger, 12).
wdef (thirteenth, ointeger, 13).
wdef (fourteenth, ointeger, 14).
wdef(fifteenth,ointeger,15).
wdef(sixteenth,ointeger, 16).
wdef(seventeenth,ointeger,17).
wdef (eighteenth, ointeger, 18).
wdef (ninteenth, ointeger, 19).
wdef(triple, quantity, triple).
wdef(twentieth,ointeger,20).
wdef (thirtieth, ointeger, 30).
wdef(single, quantity, 1).
wdef(solitary, quantity, 1).
wdef(frequency, grammar, frequency).*/
wdef ( .', grammar, '.').
.wdef(';',grammar,';').
wdef('/',grammar,'/').
wdef(':',grammar,':').
wdef('?',certainty,'moderate certainty').
wdef('+',certainty,'high certainty').
wdef('''',grammar,'''').
wdef (once, freq, 1).
wdef(times, grammar, x).
```

wdef(twice, freq, 2).

```
% lexicon with lex0g containing common English words adapted from lex0 of
MedLEE%
% lexig from lex1 of MedLEE
% August 23, 1999
. CAROL FRIEDMAN
         QUEENS COLLEGE, COLUMBIA UNIVERSITY
                                                                      용
2
2
                    Version 3.0 4-01-00
                     Version 2.0 1-31-96
                     Version 1.0 1-5-92
                     SEMANTIC LEXICON FOR CLINICAL TEXT
ž
r
  The lexicon consists of several files:
ક
     lex0g.pl: single word closed classes
8
     lexig.pl: single word - general modifier type words:
욯
    wdef(category,target).
         word - is the name of the word being categorized;
*
         category - is the semantic category for the word
         target - is the canonical/standard form for the word
                    words which are synonyms should be assigned the same
                    canonical form.
                                                                       ક
   multi-word phrases are categorized as follows:
                                                                       ક
    phrase (word, category, phrase, target).
                                                                      욯
                                                                       욯
   Semantic Categories:
       certainty "possible"
£
              canonical values limited to: moderate - for possible
                                          high - for high possible
8
                                          low - for low possible
2
       conj - relational operators "and", "or", which connect one finding %
              to another finding
8
       neg - negation "no", "not"
۶Ł
       quant - for quantitative information "many"
:-unknown(_,fail).
:-ensure_loaded([nsphrase,lex0g,lex1g,lexsemact,lexsyn,lexsub]).
```

*/

```
% definitions kept from MedLEE lexicon - lex1.pl
wdef(be, vbe, 'high certainty').
wdef (been, vbe, 'high certainty').
wdef(being, vbe, 'high certainty').
wdef(was, vbe, 'high certainty').
wdef(is, vbe, 'high certainty').
wdef(were, vbe, 'high certainty').
/*
wdef (became, vcertainty, 'high certainty').
wdef (become, vcertainty, 'high certainty').
wdef (becomes, vcertainty, 'high certainty').
wdef(becoming, vcertainty, 'high certainty').
                             put in action lexicon
wdef (changed, change, change).
wdef (changes, change , change) .
wdef (changing, change, change).
wdef (necessarily, certainty, 'high certainty').
wdef (necessary, vrecommend, recommended).
wdef (necessitate, vstatus, need).
wdef (necessitated, vstatus, need) .
wdef (necessitating, vstatus, need).
wdef (necessitates, vstatus, need) .
wdef (need, vstatus, need) .
wdef (needed, vstatus, need).
wdef (needing, vstatus, need).
wdef (needs, vstatus, need).
```

28

```
% file ml parser.pl
:- multifile(phrase/5).
:- multifile(wdef/3).
:-unknown( ,fail).
% Load in program components - library components are part of Prolog
:- ensure loaded([library(basics), library(not), library(lists),
   library(readin), library(strings), library(ctypes), library(readconst),
   library(date), library(listparts), library(sets).
   radrec, radpardb, useful, util, tagging, lexicon, gengram]).
%: - initialization run.
%run :- on exception(Error, processrun, stop(Error)).
runtime_entry(start) :- processrun.
runtime_entry(abort) :- halt.
% process report
processrun :- process, halt.
%stop(Error) :-
    told.
    write(user_error, 'Error: '), write(user_error, Error), halt.
% get user supplied parameters and process report
process :-
get_args(Mode,Infile,Outfile,Prb,Undefs,Protocol), !,
           (Examtype = []; % must have a domain
            process (Infile, Outfile, Prb, Undefs)).
% open Infile (text input) and process
process(Infile,Outfile,Prb,Undefs) :-
           see (Infile), seen, see (Infile),
           on exception (Error,
           test_genome (Outfile, Prb, Undefs),
               app erro( ,Outfile,Error)),
           closefiles (Outfile, Prb, Undefs) .
process(_,Outfile,_,_) :-
        app_err(_,Outfile,'Program failed').
app_err0(_,Output,Error) :-
       tell(Output),
       write('<error>'),
       write('Prolog Error occurred: '),
       app_err(_,Output,Error).
app_errl(_,Output,Error) :-
       tell (Output),
       write('<error>'),
       write('Error in input: '),
       app_err(_,Output,Error).
app_err(_,Output,Error) :-
       tell (Output),
       write (Error), write ('</error>'), nl.
closefiles (Outfile, Errfile, Unfile) :-
      tell(Outfile), told,
      (Errfile = []; tell(Errfile), told),
      (Unfile = []; tell(Unfile), told).
```

```
* Argument options - get user defined arguments
$ -p ProbFile (otherwise default is problem messages are not written to file)
% -i Infile (if input is supplied by file and not standard input
* -s Section (default is impression)
% -m Mode (default is relax; the three choices are strict, relax, skip)
% -o Outfile (if output should be file and not standard output)
* -? Provide list of default arguments
% -u Undefs (otherwise default is - undefined messages are not written
ક
      to a file)
get_args(Mode,Infile,Outfile,Prbfile,Undefs,Protocol) :-
    unix(args(Args)),
  (Args = [], !, writesyntax;
  Args = ['?'],!, writesyntax;
Args = [X|Rest], !,
   set_args([X|Rest], Mode, Infile, Outfile, Prbfile, Undefs, Protocol)).
writesyntax :-
     write(user_error, 'geneparser [-m Mode]'),
    nl (user error),
    write(user error,'
                                  {-t Outtype} [-p Probfile] [-u Undefs]'),
    nl (user_error),
                                [-i Infile] [-o Outfile]'),
     write(user error,'
    nl(user_error).
```

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```
% nsphrase.pl - contains words/phrases that are ignored
nosem(both, [both]).
nosem(however, [however]).
nosem(selectively, [selectively]).
nosem(specifically, [specifically]).
nosem(the, [the]).
nosem(a, [a]).
```

```
% file radpardb.pl
% June 25, 1999
% fail an unknown predicate
:-unknown(_,fail).
:- op(900, fy, [not,once]). % same priority and type as \+
:- op(700, xfx, [\=, -=]). % same priority and type as = or ==
:- dynamic(sentno/1).
% \sem\radpardb.pl
*parse_sentences(+Beg,-Fmt,-ParseErrors,-Undefineds,-Unsents,+Section,
                 +UserMode, +Examtype, Sentno, Outsno, IncSno)
        Beg is list of sentences, Fmt is list of target forms,
£
        ParseErrors are a list of sentences which could not parse,
        Undefineds is a list of undefined words in sentence
        Unsents is a list of sentence containing undefined words
        Section is the section of the examination, UserMode is the
        parsing mode specified by user,
윰
        Examtype is the domain (type of exam)
        Sentno is the number of the starting sentence
        Outsno is the last sentence number + 1
        IncSno is the amount that the sentence number should be increased
             (i.e. it is 1 when called by parse sects and 0 when in
               recovery mode)
     Each sentence is parsed independently.
parse_sentences([],[],[],[],[],[],-,-,-,-) :- !. %no more sentences
parse sentences (Beg, Fmtlist, Outfail, Outundefs, OutunSents,
                 Section, UserMode, Examtype, _,_, IncSno) :-
    get_sentence(Beg,S,Rest), !,
    ( isidentifier(S), !, % ignore identifier sentences - parse remainder
      parse sentences (Rest, Fmt1, Outfail, Outundefs, OutunSents,
                 Section, UserMode, Examtype, _, _, IncSno), !,
       (outputform(htext), S \= ['.'], !, IncSno \= 0, %0 means in recovery
mode
        append([[[sentence,S]]],Fmt1,Fmtlist);
        Fmtlist = Fmtl
      % ( IncSno = 0, !; % on same sentence in recovery mode
      % sentno(Sno), NewSentno is Sno + IncSno,
% retract(sentno(_)), assert(sentno(NewSentno))
      88),
    % Incsno = 1, write('***'), write_list(S,3,_), nl, !,
     % Incsno = 0,
      preprocess(S,Bs,Undef,Semlist,strict), % bracket and check for undefineds
      parse_modes(S,Bs,Semlist,Fmtl,Errors,Undef,Unsents,Section,Writefail,
                  Examtype, UserMode, IncSno), % parse first sentence
      parse sentences (Rest, Fmt2, Moreerrors, Moreundefs, MoreUnSents,
                  Section, UserMode, Examtype, _, _, IncSno), } parse remaining
      append(Errors, Moreerrors, Outfail),
                                               * Combine failures
      (outputform(htext),
            (Fmt1 \= [], IncSno \= 0,
             !, append([Fmt1],Fmt2,Fmtlist); % add extra bracket for 1st
             Fmt2 = [], Fmtlist = Fmtl , !
```

```
append (Fmt1, Fmt2, Fmtlist)
                     % Combine targets
      append (Unsents, MoreUnSents, OutunSents), % Combine sentences
                                          % Combine undefined words
      append (Undef, Moreundefs, Outundefs)
%parse modes(+S,+Bs,+Semlist,-Fmt,-Failures,+Undef,-Unsents,+Section,
     +WriteMessage, +Examtype, +Mode, +IncSno)
        S is original sentence; Bs is sentence after lexical lookup
        Semlist is list of semantic categories in sentence
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        Fmt is formatted output,
        Failures is list of sentences/fragments which could not be parsed.
£
ş
        Undef are words not in lexicon, Unsents are sentences containing
                undefined words
        Section is name of section being processed
        WriteMessage is message returned from doresult (in case doresult fails)
        Examtype is domain, Mode is user specified mode
*
        IncSno is 0 if this is a fragment of a sentence that was already
                parsed - but unsuccessfully; is 1 if this is a new sentence
* Best possible - try to get the most accurate parse possible trying
% all alternative strategies in turn if neccessary
% All words in sentence are defined
parse modes (S, Bs, Semlist, Fmt, Errors, [], [], Section.no, Examtype, Pmode,
      (Pmode = bpseg, Pmodemod = mode2, !; %in recovery mode
       Pmode = bpseg2, Pmodemod = mode2, !;-
       Pmode = bpseg3, Pmodemod = mode2, !;
       Pmode = bpskip, Pmodemod = mode4, !; %in recovery mode
        % in user specified parse mode - don't parse in mode 5 or keyword
       Pmode \= keyword, Pmode \= mode5,
       Pmodemod = model
      dosent(S,Bs,SemList,Fmtl,Message,Section,_,Examtype,Pmodemod,_),!, %
strict first
      recovery(_,S,Bs,Semlist,Fmt2,Message,Errors,[],[],Section,
                 Pmode, Examtype, _), % try alternative modes if neccy
      (outputform(htext), Inc \= 0, !, append([[[sentence,S]],Fmt1,Fmt2],Fmt);
       append (Fmt1, Fmt2, Fmt)
% alternative strategies if have undefined words
parse_modes(S,Bs,Semlist,Fmt,Errors,Undef,Unsents,Section,no,Examtype,
             Pmode, Inc) :-
     Undef \= [],
     recovery(_,S,Bs,Semlist,Fmtl,yes,Errors,Undef,Unsents,Section,
                Pmode, Examtype, _), % try alternatives if have undefineds
     (outputform(htext), Inc\= 0, !, append([[sentence,S]],Fmt1,Fmt);
     Fmt = Fmt1
     ).
% key word strategy is fastest but least reliable;
parse modes (S. Bs, Semlist, Fmt, Errors, Undef, Unsents, Section, no, Examtype,
             Pmode, Inc) :-
    (Pmode = keyword; Pmode = mode5
     ; Pmode = mode5),
     recovery (5, S, S, Semlist, Fmtl, yes, Errors, Undef, Unsents, Section, Pmode,
               Examtype,_),
     (outputform(htext), Inc \= 0, !, append([[sentence,S]],Fmt1,Fmt);
```

```
Fmt1 = Fmt
% Parsing/Recovery modes
% parse_modes(+Level,+S,+Bs,+Sem,-Fmt,+Failed,+Undef,+Unsents,+Section,
             +Pmode, +Examtype, _)
    Level is the recovery level of the predicate
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   S is the original sentence list
욯
   Bs is the
   Sem is the list of semantic categories in the sentence
ક
   Fmt is the formatted output for the sentence
ž
   Failed is 'yes' if the parse was unsuccessful, and 'no' otherwise
ş.
   Undef is a list of words in sentence which are undefined (not in lexicon)
٤
2
   Unsents are the lists of sentences/segments which could not be parsed.
  Section is the section of the report
ž
8
   Pmode is the user specified parse mode
  Examtype is the domain
% mode 1 is the strictest parsing mode - the parser succeeded for the complete
        original sentence using the grammar; all words in original sentence
8
        are defined in lexicon
* mode 1 - alternative not needed because parse succeeded
recovery(1,_,_,[],no,[],Undef,Unsents,_,_,_,] :-!.
         - no alternative strategy allowed in mode 1
8
           in case where there are no undefineds, Noparse is S
recovery(1,S,_,_,[],yes,S,[],[],_,Pmode,_,_) :-
        Pmode = strict; Pmode = model, !.
           in case there are undefineds, Unsents is S
recovery(1,S,_,_,[],yes,Noparse,Undef,Unsents,_,Pmode,_,_) :-
        (Pmode = strict; Pmode = 'model'),
        Undef \= [], Unsents = S, Noparse = [], !.
recovery(1,S,_,Semlist,[],yes,S,_,_,_,_,) :-
* sentence contains no relev. information, don't try to recover
     \+ (subtype(finding,Semlist); subtype(time,Semlist)), !.
% mode 4 - skip undefined words and try to parse according to mode 1
recovery(4,S,_,_,Fmt,yes,Errors,Undef,[],Sect,Pmode,Examtype,_) :-
        Undef \= [],
         (Pmode = bp; Pmode = mode4;
          Pmode = bpseg; Pmode = bpskip; Pmode = mode4
         preprocess (S,Bs, ,Semlist,bpskip),
         dosent(S,Bs,Semlist,Fmt1,Message,Sect,_,Examtype,mode4,_),!,
         recovery(_,Bs,Bs,Semlist,Fmt2,Message,Errors,[],[],Sect,
                     bpskip, Examtype, Sentno), % try alternatives if neccy
           append (Fmt1, Fmt2, Fmt).
% mode 3 - try longest parsed segment; partition rest of
            sentence using mode 5 for parse mode bp
recovery(3,S,Bs,_,Fmt,yes,Errors,Undef,Unsents,Sect,Pmode,Examtype,_) :-
         % allowable modes for choosing longest segment
         (Pmode = bp; Pmode = bpskip;
         Pmode = skip; Pmode = mode3; Pmode = mode4;
         Pmode = bpseg3; Pmode = bpseg
         (Pmode = bpskip, Pmodemod = mode4 3;
        Pmodemod = mode3
        ),
        checkst(sem_pattern,_,s,Target,Bs,Rest), %check symbol table
```

```
$dooresult(Target, Fmt1, Examtype, Sect, Pmodemod, _).
         formatresult (Target, Pmodemod, Fmt1),
         (Pmode = mode3, Fmtlist = [], Errors = Rest;
         recovery(5,Rest,Rest,_,Fmtlist,yes,Errors,Undef,Unsents,Sect,
                        Pmode, Examtype, _)
         append (Fmt1, Fmtlist, Fmt).
% mode 2 segments sentence using word barrier methods. This mode is tried if
           parse failed for original sentence/or there are undefined words
            segment sentence using word barriers
recovery (2, S, _, _, Fmt, yes, Errors, Undef, Unsents, Sect, Pmode, Examtype, _) :-
         (Pmode = bp; Pmode = bpskip; Pmode ≈ mode2; Pmode = skip;
          Pmode = mode2; Pmode = mode3; Pmode = mode4;
          Pmode = bpseg; Pmode = bpseg2;
          Pmode = bpseg3
         segmentandparse(S,Fmt,Errors,Unsents,Sect,Pmode,Examtype,_),!.
% mode 5 - try to partition sentences by findings
% when a finding in sentence is found, go left until first
    modifier is found (if 2 findings are next to each other, 2nd one
    is considered the finding and 1st is considered the modifier)
    Repeat searching for successive findings using this method
recovery(5,[],[],_,[],_,[],_,_,_,_) :- !.
recovery (5, S, Bs, _, Fmt, yes, Errors, Undef, Unsents, Sect,
               Pmode, Examtype, _) :-
         (Pmode = bp; Pmode = bpskip; Pmode = bpseg; Pmode = keymode;
          Pmode = mode5; Pmode = negmode
          preprocess(S,Bs1,_,_,bpskip), % skip undefined words
          actionfindingseg(Bs1, Fseg, Before), !, % get segment containing finding
          (Fseg = [], Errors = S, !; % no finding to segment
           $Before = [], Errors = Bs, Fmtl = [], !; % this part was tried
           preprocess (Fseg, Bseg, _, Semlist, bpskip),
           dosent (Fseg, Bseg, Semlist, Fmt1, Message, Sect, _, Examtype,
                   mode5,_) % try to parse finding segment
           (Before = [], Before1 = [], Message = yes, !; % no segmenting yet -
skip beg.
            Message = yes, Beforel = Before, !; %don't add '.'; have to skip
more
            append(Before,['.'],Beforel)
           ),
           ( Fseg = [], Fmt = [], !; % no finding left in sent. - don't recover
           recoverrest (Fseg, _, Beforel, Fmt2, Message, Errors,
                     Sect, Newmode, Examtype, ),
            % recover remainder
            append (Fmt1, Fmt2, Fmt)
% nothing could be recovered; all input -> Errors ; Format is []
recovery(_,Sents,_,_,[],yes,Sents,Undef,[],_,_,_).
% part of phrase was skipped, add period and treated skipped part as a
% sentence
% recoverrest(+Segment,+Semlist,+Before,-Fmt,+Message,-Failures,+Section,
        +Mode, +Examtype, _)
        Segment is part of sentence with a finding
```

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        Semlist is a list of semantic categories for that sentence part
¥
        Before is the part of sentence before Segment
        Fmt is the format for this segment
ŧ
        Message is 'no' if there is no segmantic information to be recovered
욯
                Message is 'yes' otherwise
ક
ž
        Failures are lists of segment(s) that could not be parsed successfully
g.
        Section is section being processed, Mode is user specified parsing mode
        Examtype is domain
recoverrest(_,_,Before,[],no,Beforel,_,_,_,) :-
  (Before = [], Before1 = [], !; % nothing was skipped
   append(Before,['.'],Before1)
% nothing left to recover; write phrase that was skipped
recoverrest([],_,Before,[],yes,Before1,_,_,_) :-
   (Before = [], Before1 = [], !;
   append(Before, ['.'], Beforel)
   ), !.
% can recover partial parse
recoverrest (Bs, ,Before,Fmt,yes,Errors,Sect,Pmode,Examtype,_) :-
         checkst(sem_pattern,_,s,Target,Bs,Restseg), % recover from symbol tab.
         $doresult(Target, Fmtl, Examtype, Sect, mode5, _),
          formatresult(Target, mode5, Fmt1),
         recovery(5,Restseg,Rest,_,Fmt2,yes,Error2,
                    [], [], Sect, Pmode, Examtype, ),
         append (Fmt1, Fmt2, Fmt),
         (Before = [], Errors = Error2, !;
                                             %nothing skipped to add '.' to
          append(Before, ['.'|Error2], Errors)
% cannot recover partial parse - skip first element and retry
% if 1st element is a negation semantic type, skip 2nd element instead
ē.
      Handles case where 1st element is a negation, certainty or status
g.
        add 2nd element to unparsed sentences list (enlcosed in angle brackets).
recoverrest([X,Y|Restseg],_,Beforel,Fmt,yes,Errors,
                     Sect, Pmode, Examtype, ) :-
         foundword(X,Seml,Tar),
         ( member(Sem1, [neg, certainty, vcertainty, vconn, status, vstatus]);
           Sem1 = p, Tar = [\_,conn]
         % (Mod = neg; Mod = certainty; Mod = status; Mod = vcertainty), % leave
this mod in
          preprocess([X|Restseg],Fseg0,_,_,bpskip), % skip undefined words
          findingseg(Fseg0,Fseg,Before2), !, % get finding seg
          (Fseg = [], Errors = [X,Y|Restseg], Fmt = []; % no finding
           preprocess(Fseg,Bseg,_,Restsem,bpskip), % skip undefined words
           dosent(Fseg,Bseg,Restsem,Fmt1,Message,Sect,_,Examtype,
                   mode5,_), % try to parse finding segment
           recoverrest(Fseg,_,[Y|Before2],Fmt2,Message,Error2,
                     Sect, negmode, Examtype, _), % recover remainder
           (Before1 = [], Errors = Error2, !;
            append(Before1, [. | Error2], Errors)
           ).
           append (Fmt1, Fmt2, Fmt)
  skip 1st element; enclose it in brackets
recoverrest([X|Restseg],_,Beforel,Fmt,yes,Errors,
                Sect, Pmode, Examtype, _) :-
          preprocess(Restseg, Fseg0, _, _, bpskip),
```

```
findingseg (Fseq0, Fseq, Before2), !, % get finding seg
          append (Before1, [X | Before2], Before),
           (Fseg = [], Errors = [X|Restseg], Fmt = []; % no finding
           preprocess (Fseg, Bseg, _, Restsem, bpskip),
          dosent (Fseg, Bseg, Restsem, Fmt1, Message, Sect, _, Examtype,
                    mode5,_), % try to parse finding segment
          recoverrest (Fseg, _, Before, Fmt2, Message, Errors,
                      Sect, Newmode, Examtype, ), % recover remainder
          append(Fmt1,Fmt2,Fmt)
          ١.
t no semantic information left; return Errors
recoverrest([X]Restseg],[];Before1,Fmt,yes,[X]Restseg],
                Sect, Pmode, Examtype, ).
%dosent(+S,+Bs,+Semlist,-Fmtlist,+Message,+Section,+WriteMessage,+Examtype,
        +Mode)
*
å
       S is original list of words in sentence; Bs is list after lexical lookup
       Semlist is list of semantic categories corresponding to Bs
       Fmtlist is list of target forms for sentence
       Message is 'yes' if the output from parser signals a failure,
                and 'no' otherwise
       Section is section of examination being processed
       WriteMessage signals whether an error occurred in generating target form
       Examtype is the domain, and Mode is the user specified mode of parsing
% Parse sentence and returns target in nested format
* Handles case where sentence should be skipped because info is about
    family member or peripheral to patient
dosent(S,_,Semlist,[],Error,_,_,_,_) :-
  skipsentence(S, Semlist, Error), !.
dosent (S, Bs, Semlist, Fmtlist, Errormsq, Section, Writefail, Examtype, Mode, ) :-
   attemptparse (P, Bs, sentence, Semlist, Section, Atotal),
   ( P = [failure], Errormsg = yes, Writefail = no, ! % parse failure
      P = [], Errormsg = no, Writefail = no, Fmtlist = {], ! % empty target
      %doresult(P,Fmtlist,Examtype,Section,Mode, ),
        formatresult (P, Mode, Fmtlist),
        Errormsg = no, Writefail = no,!
      Errormsg = yes, Writefail = yes, !
   ) .
%parse_sentences(Beg, Beg, [], [], _, _, ) :- !.
$ attemptparse(-P,+Bs,+Structure,+Semlist,-Ftype,-Total)
        P is output from parser
        Bs is list of words in sentence after lexical lookup
        Structure is name of structure to be parsed
ş.
        Semlist is list of semantic categories corresponding to elements in Bs
        Total is number of times parser reached sem sent in grammar;
                 where sem_sent is highest level predicate in grammar
% don't parse if sentence consists of only '.' or ';'
attemptparse([],Bs,_,_,,_,) :-
Bs = ['.']; Bs = [';'].
% if a template exists for whole sentence, get parse from it
```

```
attemptparse(P,Bs,sentence,_,_,) :-
   Bs = [X,','], is list (X), the whole sentence is a finding
   find sem_sent(P,X), !.
% parses and retracts wellformed string table - parses sentence
attemptparse(P,Bs,sentence,Semlist,Ftype,Atotal) :-
   retractall(wfst(_,_,_,_,_)),
   retractall(addstotal()),
   sem sent(P, Semlist, Atotal, Bs, []), !.
% parses and retracts wellformed string table - parses bodypart only
attemptparse(P,Bs,bodypart,_,_,) :-
   sem bodyloc(P,Bs,[]),
   retractall(wfst(_,_,_,_,_)), !.
*segmentandparse(+Sentences,-Fmtlist,-Failures,-Unsent,+Section,+Mode,
        +Examtype, +Sentno)
ž
ક
        Sentences is list of sentence segments.
        Fmtlist consists of the formatted output for the segments
8
        Failures is the list of unparsed segments.
        Unsent is the list of segments with undefined words.
        Section is the section being processed, Mode is the user specified mode
        Examtype is the domain and Sentno is the sentence id.
\label{eq:segmentandparse} \begin{split} & \text{segmentandparse}([],[],[],[],\_,\_,\_) :- \ ! \cdot \\ & \text{segmentandparse}(\text{Sentences},\text{Fmtlist},\text{Failures},\text{UnSent},\text{Section},\text{Mode}, \end{split}
                    Examtype, Sentno) :-
     get_sentence(Sentences, S, Rest), !, %sentence to segment
     preprocess(S,S1,_,Semlist,Mode), !,
      (Mode = mode2, NewPmode = bpseg2, !;
      Mode = mode3, NewPmode = bpseg3, !;
      NewPmode = bpseg
     ),
      ( segment1(S1, Segs, [], seg), !,
          parse sentences (Segs, Fmt1, Fails, , Un1, Section, NewPmode, Examtype,
                              Sentno, Sentno, 0), !
       ; segment2(S1, Segs, [], seg), !,
         parse_sentences(Segs,Fmt1,Fails,_,Un1,Section,NewPmode,Examtype,
                              Sentno, Sentno, 0), !
       ; segment3(S1, Segs,[], Negstatus, seg), !,
          parse_sentences(Segs,Fmt1,Fails,_,Un1,Section,NewPmode,Examtype,
                              Sentno, Sentno, 0), !
       % fails if cannot segment sentence; otherwise segments remainder
      segmentandparse (Rest, Fmt2, Nexterrors, NextUns, Section, Mode,
                          Examtype, Sentno),
      append (Fmt1, Fmt2, Fmtlist),
      append (Un1, NextUns, UnSent),
      append (Fails, Nexterrors, Failures), !.
$segment1(+S,-Segs,+Beg,+Message)
8
         S is list of words in sentence
왐
        Segs consists of sentence segments as separate sentences
         Beg is list of words in sentence prior to the current portion of sentenc
¥
        Message is 'seg' if segmenting succeeded and 'noseg' otherwise
segment1([],[],_,noseg) :- !.
% segment sentence at connect phrase/word or at most conjunctions
% if negation precedes, restore negation
```

```
segment1([X|Rest],['.','<eos>'|Rem],Beg,seg) :-
     \+ sem_endmark(Rest, []), % don't segment if at end already
     foundword(X,Sem,Target), % get semantic classification and target
     ( X = nor, append([no], Rest, Rem) % ok to segment at nor
      ;X = without, append([no],Rest,Rem) % ok to segment at without
      %;X = ':', Rest = Rem
      ; Sem = neg, Rest = [Next|Rest2], % have negation; test word after
        foundword(Next,Sem2,Target2), % for connective - add back negation
         testforconn(Next, Sem2, Target2), Rem = [X | Rest2]
      ; testforconn(X,Sem,Target), Rest = Rem
     ) .
segment1([X|Rest],[X|Newrest],Start,Seg) :-
       append(Start,[X],Beg), % part before segmentation
       segment1 (Rest, Newrest, Beg, Seg).
testforconn(X,Sem,Target) :-
      ( Sem = p, Target = [P,conn], P\= with % segment at connective prep
      ; member(Sem, [vconn, vshow]) % segment at these types of verbs
      ; Sem = conj, \+ member(X, [and, or, ', ', '/', as])
      ١.
% segment at certain words -
segment2([],[],[],noseg) :- !.
segment2(S, Segs,[], seg) :-
        seg2 (S, Rest, Segs),
        \+ sem endmark(Rest,[]), !.
segment2([X|Rest],[X|Newrest],[],Seg) :-
       segment2 (Rest, Newrest, [], Seg).
seg2([X|Rest],Rest,['.','<eos>'|Rem]) :-
        member (X, [which, that, until, where, when, while, who,
         '(',')', between, whereby, after, before, prior,
         greater, ranging]),
        Rem = Rest, !.
segment3([],[],_,_,noseg) :- !.
% segment at conjunction - if negation preceded conjunction, add
segment3([X|Rest], Rem, Beg, Negstatus, seg) :-
       \+ sem_endmark(Rest,[]), !, % already at end of sentence
        seg3([X|Rest], Rem, Beg, Negstatus, seg), !.
seg3([X|Rest],Rem,Beg,Negstatus,seg) :-
        wdef(X,conj,_),
        member(X, [and, or, ', ']),
        (nonvar(Negstatus), Rem = ['.', Negstatus|Rest], ! %restore negation
         ; Rem = ['.','<eos>'[Rest], !
seg3([X|Rest],[X,'.','<eos>'|Rest],_,_,seg) :-
       foundword(X,age), !.
seq3([X|Rest],[X|Newrest],Start,Negstatus,Seg) :-
        ( nonvar(Negstatus), !; % 1st neg already found - continue segmenting
foundword(X,Sem,Target), !,
            ( Target = no, Negstatus = X, !;
              Sem = neg, Negstatus = X, !;
              Sem \= neg, Target \= no, !
            );
```

```
% file radrec.pl
% September 7, 1999
fail an unknown predicate
:-unknown(_,fail).
:- op(900, fy, [\+,not,once]).
                                  % same priority and type as \+
:- dynamic(domain/1).
                               % domain being processed
:- dynamic(outputform/1).
                               % form of output (needed to distinguish
                               % markup of text from formatting forms
:- dynamic(currentsect/1).
                               % section for outputting results
test genome (Outfile, Errfile, Unfile) :-
     get_inputsents([],Toklist), !, % read in and tokenize input
     (Toklist = [], !, % error condition
      app_err1(_,Outfile,'No input sent'), !
      parse_sentences(Toklist,Fmtlist,Failed,Undef,UnSent,impression,
bp,genome,_,_,0),!,
      outputresults (Fmtlist, Failed, Errfile, Undef, Unfile, UnSent, Outfile,
                    full, line, genome, 1, 0, _, exe, plain)
     ).
outputresults(FmtlistO, Failed, Errfile, Undef, Unfile, UnSent, Outfile,
               Amount, Type, Exam, Compno, DocComp, NewCompno, Caller, Protocol) :-
      tell(Outfile),
     (Protocol = sgml, !, Op = sgml;
      Caller = server, !, Op = sgml;
       Op = plain),
      (Type = nested, !, % original output form - nested findings
       write('<nested>'), new line(Op),
        write(Fmtlist), new_line(Op), write('</nested>'),
        new line (Op), !
      ).
     (Caller = server,
      write_message(Unfile,Undef,Caller,'<undefined>','</undefined>')
      Caller = exe, Undef \= [],
      write_message(Unfile,Undef,Caller,'***** Undefined Words *****',[])
    %write_highlight([],UnSent,Caller)
      true
     ),
     (Caller = server,
    write('<noparse>'),!,
    write_highlight (Undef, UnSent, Caller),
    write_highlight([],Failed,Caller), write('</noparse>')
    Caller = exe, Errfile \= [], Failed \= [],
    tell(Errfile),
    write('***** Sentences/Phrases Not Parsed *****'), nl,
     %write highlight(Undef,UnSent,Caller),
    write highlight ([], Failed, Caller)
    true
            % no Errfile to write to
   ).
% set_args: Process options
```

```
% Argument options
% -p ProbFile (otherwise default is problem messages are not written to file)
% -i Infile (if input is supplied by file and not standard input
% -m Mode (default is bp; the 6 choices are bp, model - mode5)
% -o Outfile (if output should be file and not standard output)
% -? Provide list of default arguments
% -pr Protocol - sgml or plain (default is plain)
% -u Undefs (otherwise default is - undefined messages are not written
      to a file)
set args(Args, Mode, Infile, Outfile, Prbfile, Undef, Protocol) :-
      set mode(Args, Mode), set amount(Args, Amount),
      set protocol (Args, Protocol),
      set infile(Args, Infile), set outfile(Args, Outfile),
      set_prbfile(Args,Prbfile), set_undefs(Args,Undef).
set mode(Args, Mode) :-
    (nextto('-m',M,Args); nextto(m,M,Args)), !,
    modeis(M, Mode), !.
set_mode(_,bp). % default output type
modeis(relax, mode2) :- !.
modeis(strict, model) :- !.
modeis(skip, mode4) :- !.
modeis(longest, mode3) :- !.
modeis(best,bp) :- !.
modeis(model, model) :- !.
modeis(mode2, mode2) :- !.
modeis(mode3, mode3) :- !.
modeis(mode4, mode4) :- !.
modeis(mode5, mode5) :- !.
set_protocol(Args,Protocol) :~
    (nextto('-pr',Protocol,Args); nextto('pr',Protocol,Args)),
     member(Protocol, [sgml, plain]), !.
set protocol (, plain).
set undefs(Args, Undefs) :-
    nextto('-u', Undefs, Args); nextto(u, Undefs, Args) , !. % undef file option
set_undefs(_,[]). % default is no file of undefineds created
set_infile(Args,Infile) :-
    nonvar(Infile), !; % Infile is set already
    nextto('-i', Infile, Args), !;
    nextto(i, Infile, Args), !.
set_infile( ,user_input).
                           % default is standard input
set prbfile (Args, Prbfile) :-
    nextto('-p', Prbfile, Args), !; nextto(p, Prbfile, Args), !. % prob file option
set_prbfile(_,[]). % default is no file of problems is created
set_outfile(Args,Outfile) :-
    nonvar(Outfile), !; % Outfile is already set
    nextto('-o',Outfile,Args), !; nextto(o,Outfile,Args), !. % outfile option
set_outfile(_,user_output). % default is standard output
new_line(sgml) :- write('<br>'), nl, !.
new_line(server) :- write('<br>'),nl, !.
new line (exe) :- nl.
```

```
new_line(plain) :- nl. '
write_message(_,[],exe,_,_) :- !.
write_message([],_,exe,_,] :-!.
write_message(_,[],plain,_,_) :- !.
write_message([],_,plain,_,) :- !.
write message (File, Contents, Caller, Begmsg, Endmsg) :-
   ( member(Caller,[exe,plain]), tell(File), !
    true),
   write(Begmsg), new_line(Caller),
   (Contents = []; write_list(Contents,1), new_line(Caller)
   (Endmsg = [], !;
   write(Endmsg), !, new_line(Caller)
sentend([X|_],Caller) :-
   member(X,['.',',','?']), new_line(Caller), !.
gettargets([],[]) :- !.
gettargets([ignore|Rest], [ignore|Rest]) :-!. % possibly ignore info.
gettargets([W1|Rest],[T1|Trest]) :-
     foundword(W1,_,T1),
                            % target for W1
     gettargets (Rest, Trest), !.
gettargets(W,W). % not in lexicon
isneg(X) :-
    intersect (X, [no, negative, deny, 'rule out']).
writeoutsent([Word|Rest]) :-
  write(''''), write(Word), write(''''), !,
  (Word = '''', write(''''), !; true),
  (Rest \= [], write(','), !, writeoutsent(Rest), !;
   true), !.
```

```
* This file contains predicates associated with SGML tags
* nextTag(+L,Tag,-PreTag,-PostTag) is true if
      L is the starting List
*
8
      Tag is an SGML tag; it could be a variable or instantiated already
      PreTag is portion of L preceding Tag
욯
      PostTag is portion of L following Tag
%
nextTag(L, Tag, PreTag, PostTag) :-
    append(PreTag,['<',Tag,'>'|PostTag],L).
% endTag(+L,+Tag,-Pre,-Post) is true if
      L is the starting list
ě
¥
      Tag is the SGML end tag
      Pre is the portion of L preceding the end of tag
ş
      Post is the portion of L following the end of tag
용
endTag(L, Tag, Pre, Post) :-
    append([Pre,['<','/',Tag,'>'],Post],L).
% enclosedPart(+L,+Tag,-Enclosed) is true if
      L is the starting List; it is assumed that L is portion of some
ક
윰
      list that follows a begin tag - i.e. '<', Tag L
¥
      Tag is the SGML tag
      Enclosed is the portion of text enclosed in tag; not including
¥.
윰
     end tag.
enclosed, Post) :-
    endTag(L, Tag, Enclosed, Post).
```

```
% file useful.pl - lexical lookup and utility tools
:-unknown(_,fail).
:-dynamic(sentence/1).
:- op(900, fy, [not,once]). % same priority and type as \+
% useful.pl February 21, 1992
% preprocess(+S,+Bs1,-U,-Sem3,+Mode): preprocesses sentence to
           bracket lexical phrases and remove words/phrases in
           special db of noise words (nosem in nsphrase.pl db)
욯
        S is original sentence
뫞
       Bsl is preprocessed sentence
       U is list of undefined words in sentence
        Mode is mode of process - in skip mode undefined words are removed
         from preprocessed sentence
preprocess (SO, Bsl, U, Sem3, Mode) :-
                                      %cfnew
                  % if beginning is 'A)' ignore
 checkbeg(S0,S),
 checkphrase(S,S1,Sem1), % bracket all phrases in phrasal lexicon first
  checklist(S1,U1,Bs,Sem2,Mode), % check that all words are in lexicon, remove
  checklist (Bs, U, Bs1, Sem3, Mode). % check for phrases after non-sem are removed
 %append (Sem1, Sem2, Sem1),
%append(Seml, Sem3, Semlist),
 tunion(U1,U2,U).
% found checks if word X is defined as a single word, or if X starts a defined
% phrase
foundword(X) :-
    wdef(X, _, _), !.
foundword(X) :-
      semw(X,_,_,_),!.
%definition from tagged input
foundword(X) :-
   phr(X,_,_,_), !.
foundword([X Rest]) :-
      Rest \= [],
    phrasal(X,_,[X|Rest],_), !.
% 3/99 added foundword to search the new semact.pl lexicon
% phrasal using semp was added to util.lp
% found/2 returns semantic cat. of word
foundword(X,Sem) :-
    wdef(X,Sem,_).
foundword (X, Sem) :-
      semw(X,Sem,_,_).
%definition from tagged input
foundword(X,Sem) :-
     phr(X, Sem, [], _).
foundword([X|Rest],Sem) :-
    phrasal(X,Sem,[X|Rest],_).
% found/3 returns semantic cat. and target form
foundword(X, Sem, Form) :-
    wdef(X,Sem,Form).
foundword(X,Sem,Form) :-
     semw(X, Sem, Form, _).
%definition from tagged input
foundword(X,Sem,Form,_) :-
     phr(X, Sem, [], Form).
foundword([X|Rest], Sem, Form) :-
```

```
phrasal (X, Sem, [X|Rest], Form).
%collectsem(+Word,-Sem): Sem is the list of semantic classes corresponding
   to Word
collectsem (Word, Sem) :-
    setof(X, foundword(Word, X), Sem).
% missing checks if a word present in a sentence is defined
missing(X) :-
     member (X,S),
     not foundword(X).
% checkbeg(+S0,-S) checks beginning of sentence; if it begins with a letter or
% number followed by a ')', that part is skipped
checkbeg((X,')'|Rest],Rest) :- !.
checkbeg(X,X).
% checks every word in a list to see if it is defined; creates
% a new list of words not defined, and a new list of sentence
% where phrases are bracketed.
checklist([],[],[],[],_).
* if X is a list it has already been identified as a phrase in phrasal lex
checklist([X]Rest], Undef, Newrest, Semlist, Mode) :-
     is list(X),
     check_no_sem([X|Rest],Rest1,_),
     checklist (Restl, Undef, Newrest, Semlist, Mode), !. %is phrase part of nosem
checklist((X|Rest], Undef, (X|Newrest), Semlist, Mode) :-
     %collectsem(X,Sem),
     is_list(X), X = \{W1 | Tail\},
     phrasal(W1,Sem,X,_),
     checklist (Rest, Undef, Newrest, Sem2, Mode) , !,
     append([Sem],Sem2,Semlist).
checklist([without|Rest],Undef,Newrest,Semlist,Mode) :-
     checklist([with, no | Rest], Undef, Newrest, Semlist, Mode).
this problem has to be fixed in preprocessor
% check for a number with a ',' - "11,200" and fix it
*checklist([X,',',Y|Rest],Undef,[N|Newrest],[number|Semlist],Mode) :-
     number(X), number(Y), N is X * 1000 + Y, !,
     checklist (Rest, Undef, Newrest, Semlist, Mode), !.
t check for a literal number
                                *cfnew
checklist([X|Rest], Undef, [X|Newrest], [number|Semlist], Mode) :-
     number(X)
     checklist (Rest, Undef, Newrest, Semlist, Mode), !.
beginning of List is a prefix of a phrase that is a complete finding
checklist(List,Undef,[Phrase|Newrest],(cfinding|Semlist],Mode) :-
     check sem finding(List, Rest, Phrase),
     checklist(Rest, Undef, Newrest, Semlist, Mode) , !.
beginning of List is a prefix of a phrase that is in nosemantic lexicon
checklist(List, Undef, Newrest, Semlist, Mode) :-
     check_no_sem(List, Rest, Phrase),
     checklist(Rest, Undef, Newrest, Semlist, Mode), !.
$ beginning of List is a prefix of a phrase that is in phrasal lexicon
checklist(List, Undef, [Phrase | Newrest], Semlist, Mode) :-
     get_longest_sem(List,Rest,Phrase,Sem),
     %check sem(List,Rest,Phrase,Sem), %change to get longest phrase
     checklist (Rest, Undef, Newrest, Sem2, Mode), !,
     append (Sem, Sem2, Semlist).
% beginning of List is a single word that is in semantic lexicon
checklist([X|Rest], Undef, [X|Newrest], Semlist, Mode):-
```

```
collectsem(X, Sem), !,
     %foundword(X,Sem), !,
     checklist(Rest, Undef, Newrest, Sem2, Mode), !,
     append (Sem, Sem2, Semlist).
% beginning of List is an undefined word
checklist([X Rest], Undefs, Nrest, Semlist, Mode):-
     checklist (Rest, Undef, Newrest, Semlist, Mode),
     (member(X,Undef), !; Undefs = [X|Undef], !),
     (Mode = skip, !, Nrest = Newrest;
      Mode = bpskip, !, Nrest = Newrest;
      Nrest = [X | Newrest]), !.
% if beginning is a number followed by a . followed by a non number
% skip;
        *cfnew
checkphrase([X,.],[X,.],[]) :- !.
checkphrase({X,.,Z|Rest},Y,Semlist) :-
     number(X), not(number(Z)), checkphrase(Rest,Y,Semlist), !.
% beginning of List is a prefix of a phrase that is a complete finding
% or a phrase in phrasal lexicon
checkphrase(List, [Phrase|Newrest], Semlist) :-
     (check_sem_finding(List,Rest,Phrase), Sem = [cfinding];
      get longest sem(List, Rest, Phrase, Sem)
     ), !,
     %check sem(List, Rest, Phrase, Sem)), !,
     checkphrase (Rest, Newrest, Sem2) , !,
     append (Sem, Sem2, Semlist).
checkphrase([W|Rest],[W|Newrest],Semlist) :-
     checkphrase (Rest, Newrest, Semlist).
checkphrase([],[],[]).
check sem finding([W|Tail], Tail, W) :-
           W = [W1|Rest], % W is bracketed already
           sem finding sent (W1, W, ).
check sem finding([W|Tail], Sfinal, Phrase) :-
           sem finding sent (W, Phrase, ),
           begsublist (Phrase, [W Tail], Sfinal), !.
sem_finding_sent(_,_,_) :- fail.
% check_no sem(+Sent,-Rest,-Phrase): removes Phrase from Sent resulting
     in Rest if Sent begins with a phrase in nosem (non-semantic list).
check_no_sem([W|Tail],Sfinal,Phrase) :-
           nosem(W,Phrase), *phrase beg. with W that should be removed
           begsublist (Phrase, [W|Tail], S1),
           remove_comma(S1,Sfinal), !. % remove "," if it is next
%get_longest_sem(+Sent,-Rest,-Phrase,-Sem): Phrase is longest phrase that is
% a prefix of Sent; Rest is remainder and Sem is list of semantic classes
get_longest_sem(Sent,Rest,Phrase,[Sem]) :-
        setof(X,check sem(Sent,X),L), % set of Phrases
                                        % Phrase with maximum length
        maxphrase(L,[],Phrase,0),
                                        % rest of sentence after Phrase
        append(Phrase, Rest, Sent),
        foundword (Phrase, Sem).
% check_sem(+Sent,-Rest,-Phrase,-Sem): checks if phrase beginning with
        Sent is in phrasal lexicon; Rest is the remainder of Sent after phrase
        Sem is the semantic class
*
check sem([W|Tail], Rest, Phrase, Sem) :-
           phrasal(W,Sem,Phrase,_),
begsublist(Phrase,[W|Tail],Rest).
```

```
% file util.pl
fail an unknown predicate
:-unknown(_,fail).
:- dynamic(wfst/6).
:- dynamic (addstotal/1).
:- dynamic (paragno/1).
:- dynamic(sectno/1).
:- dynamic(phr/4).
% wfst(+Rule,+Number,+Res,+Fmt,+S0,+S): well-formed symbol table
      Rule is the name of rule; Number is the option number
      Res is s for success and f for failure
¥
      Fmt is the format (for successes); for failure Fmt is []
%
      SO is the sentence position at the start of Rule
      S is the sentence position when Rule has been completed
       add to wfst
addst(Rule, Number, Res, Fmt, SO, S) :-
   assert (wfst (Rule, Number, i, Fmt, SO, S));
   assert (wfst (Rule, Number, Res, Fmt, SO, S))), !.
addst(_,_,_,_):- !. % always succeed
% checkst(+Rule,-Number,-Res,-Fmt,+S0,-S): checks to see if rule has been saved
      in wfst
8
checkst(Rule, Number, Res, Fmt, SO, S) :-
   wfst (Rule, Number, Res, Fmt, SO, S).
% beglist(L,Y) - is Y the head of list L
beglist(\{X\}, Y):- X = Y, !.
% splice(+L1,-L2) : L1 is a list of lists; L2 is merged list
splice(L1,L2) :- append(L1,L2), !.
%splice([],[]) :- !.
*splice([[]],[]) :- !.
*splice([X],X) :- !.
*splice([[] [L1],L2) :- splice(L1,L2),!.
%splice([[[]]|L1],L2) :- splice(L1,L2),!.
%splice([X[[]]],L) :- splice(X,L),!.
*splice([L1,L2],L3) :-
      append(L1, L2, L3), !.
%splice([X|L1],L2) :-
ž
       splice(L1, L3),
      append(X,L3,L2) . !.
*splicerel - works with relations which have Arg1,...,Argn.
           It splices a Splicelist in each arg of relation
splicerel (Finding, Splicelist, Spliced) :-
          splice(Splicelist, Spl),
          (Finding = [rel, X|Rest], spliceargs (Rest, Spl, Sp),
            %splice([[rel,X],Sp],Spliced),!;
```

```
append([rel,X],Sp,Spliced),!;
              *splice((Finding, Spl), Spliced) ).
              append(Finding, Sp1, Spliced)).
*spliceargs - Splices a list into each element of a list
spliceargs([],_,[]) :-!.
spliceargs([Arg1|Rest], Splicelist, Spliced) :-
           $splice([Arg1,Splicelist],Sarg1),
           append (Argl, Splicelist, Sargl),
           spliceargs (Rest, Splicelist, Srest),
           %splice([[Sarg1], Srest], Spliced).
           append([Sarg1], Srest, Spliced).
list([],[]).
list([X|[]],X).
list([X|L1],L2) :- list(L1,L3),
                   append([X],L3,L2), !.
% strip(L1,L2) removes extra square brackets from L
strip([L],L).
% B is a suffix of A and C is the difference
difflist(A,B,C) :- append(C,B,A).
% S is a sublist at beg. of L if there is a list Rest, which when appended
    to S results in L.
begsublist(S,L,Rest) :- append(S,Rest,L), !.
t checks that first element in list S has semantic category in Semlist
firstword([W1|_],Semlist) :-
    atom(W1), wdef(W1,Sem,_), % semantic category
    member (Sem, Semlist).
firstword([W1| ], Semlist) :-
    is_list(W1), phrasal(W1,Sem,_,_),
    member (Sem, Semlist).
% removes phrases from first arg that are in nsphrase - lexicon of non-sem.
phrases
remove_no_sem([],[]) :- !.
remove_no_sem([W|Tail],Sfinal) :-
          nosem(W, Phrase), %phrase beg. with W
           begsublist(Phrase,[W|Tail],S1), %remove from sentence
           remove comma(S1,S2), %remove "," if it is next
          remove no sem(S2, Sfinal), !.
remove_no_sem([W|Tail],Sfinal) :-
          remove_no_sem(Tail,S1),
          append([W],S1,Sfinal) , !.
remove_comma({','|Tail},Tail).
remove comma(S,S).
% remove_sem(+Sent,-NewSent): Sent is the original sentence, NewSent is
     stripped of all phrases that are defined in lexicon
remove sem([],[]) :- !.
remove_sem(S,NewS) :-
    remove_sem(Rest, NewS), !.
remove sem(S, NewS) :-
    check_no_sem(S,Rest,_),
                             % phrase in sent. is in nosem list - remove it
    remove_sem(Rest, NewS), !.
remove_sem([X|Tail],[X|NewS]) :-
    remove_sem(Tail,NewS), !. % not a phrase, process rest
% remove_words(+Sent,-NewSent): Sent is the original sentence, NewSent
    is stripped of all words that are in lexicon
```

```
remove words([],[]) :- !.
remove_words([X|Rest],NewRest) :-
     ( (foundword(X); number(X)),
                                     % X is defined in lexicon
       remove words (Rest, NewRest) , !;
       remove_words(Rest, New), NewRest = [X|New], ! % X is not in lexicon
%maxphrase(+ListofPhrases,+Maxin,-MaxOut,InitMaxLen) is true if
   ListofPhrase is a list of multi-word phrases,
      Maxin is phrase with maximum words so far
      MaxOut is phrase with maximum length of phrases in ListofPhrases
      InitMaxLen is length of initial phrase which is of max. length
maxphrase([],Maxin,Maxin,_) :- !. % no more phrases - maximum is same as maxin
maxphrase([P|Rest], Maxin, Maxout, InitMaxLen) :-
     length (P.Len), % length of first phrase
     ( Len > InitMaxLen, !, maxphrase(Rest,P,Maxout,Len);
       Len < InitMaxLen, !, maxphrase(Rest, Maxin, Maxout, InitMaxLen)
*acclex(Sem, W, SO, S) :-
    outputform(htext), !, acclex1(Sem, W, SO, S).
acclex(Sem, W, SO, S) :-
   acclex2 (Sem. W. SO. S).
acclex(Sem, W, SO, S) :-
   acclexss (Sem, Syn, Target, Features, SO, S).
% check lexicon for word or phrase, Target form is original W
acclex1(p, [P,C], [W|Rest], Rest) :-
         is list(W),
         find sem phrase (p, [P, C], W).
acclex1(p,[P,C],[W|S],S) :- atom(W),
                            wdef(W,p,[P,C]).
acclex1(Sem, [W], [W|Rest], Rest) :-
         is_list(W), %if bracketed list, get Sem and Code from phrasal lexicon
         find sem phrase (Sem, , W) .
acclex1(Sem, W, [W[S], S):-
                           atom(W),
                           wdef(W,Sem, ).
% check lexicon for word or phrase, Target form is taken from lexicon
%acclex2(Sem, Code, [W|Rest], Rest) :-
          is_list(W), %if bracketed list, get Sem and Code from phrasal lexicon
¥.
          find_sem_phrase(Sem, Code, W).
acclex2(Sem, Code, [W|S],S):- foundword(W, Sem, Code),
                                                             % protect against
                                            nonvar (Code) .
lex, error
find a phrase [W|Tail] in lexicon that begins with W and has category Sem
find sem phrase (Sem, Code, [W|Tail]) :-
         phrasal(W, Sem, [W|Tail], Code), % phrase and code beg. with W
         nonvar (Code) .
% case where phrase is already bracketed, look up phrase
sem finding phrasel(Code, [W|Tail], Tail) :-
         is list(W), %phrase is bracketed
         find sem sent (Code, W),
         nonvar(Code). %protect against lexical error
% case where phrase is already bracketed, look up phrase
sem finding phrase2 (Code, [W|Tail], Tail) :-
         is_list(W), %phrase is bracketed
```

```
find sem sent (Code, W).
         nonvar(Code). %protect against lexical error
Phrasal succeeds if lexicon contains phrase
phrasal (W1, Sem, Phrase, Code) :-
       phrase(W1, Sem, Phrase, Code, ). %multi-word phrase in lexicon
% added March15, 1999
phrasal (W1, Sem, Phrase, Code) :-
            semp (W1, Sem, Phrase, Code, Features).
% lexical definition from marked up input
phrasal (W1, Sem, [W1 | Tail], Code) :-
            phr(W1,Sem,Tail,Code).
acclexss(Sem, Syn, Target, Features, [W|S],S):-
            atom(W),
            semw (W, Sem, Target, Features),
            synw(W, Synclass),
            member (Synclass, Syn).
acclexss(Sem, Syn, Target, Features, [W|S],S):-
            is_list(W),
            find phrasess (W, Sem, Syn, Target, Features).
find phrasess([W1|Tail], Sem, Syn, Target, Features): -
            semp(W1, Sem, [W1 | Tail], Target, Features),
            symp(W1, [W1|Tail], Symclass),
            member (Synclass, Syn).
% lexical definition of a complete finding
find_sem_sent(Code,[W|Tail]) :-
         sem finding sent (W, [W | Tail], Code).
listify(C, [C]) :-
         atom(C), !.
listify(C,C) :-
          is_list(C), !.
% distributes left mods and right mods over list of findings creating
% list of lists of findings with mods
distributemods([],[],_,_,) :- !.
distributemods(Dist, [D1 | Tail], Lmods, Rmods, Type) :-
        distributemods(Dist2, Tail, Lmods, Rmods, Type), %distributed for remainder
        mergemods (Lmods, Rmods, Allmods),
        % Combine findings to get list of findings
        append([D],Dist2,Dist).
fixconj - if Leftmods has {certainty,no}, and Conj = or, change Conj to and.
        no A or B = no A and no B; 'denies A,B, or C' is similar.
fixconj(Leftmods,Conj,[rel,and]) :-
        (member([certainty,no],Leftmods); member([certainty.deny],Leftmods)),
        Conj = [rel,or].
fixconj(_,Conj,Conj).
         write sentences/1 inputs a PROLOG list and prints out lines
         which which are English sentences. No wrapping is done.
write_sentences([]) :- !.
write_sentences([X]) :- write(X), nl. % special sentence - section name
write_sentences(['<',p,'/','>']) :-
     write(''), nl.
                          * paragraph mark
write_sentences([X|Rest]) :-
        upper_first([X|Rest],[U|Rest]),
```

```
write(U), % First letter of first word made upper case
        %write(X),
         (X = U, chkforpunct(U,Rest), !, write_terms(Rest); % no space needed
        write(' '), write_terms(Rest)
         write_sentence/2 inputs a PROLOG list and prints out an English
         sentence wrapped. Idlen is the starting position of the sentence
*
         in the output.
*
          uses libraries ctypes, basic, not
write sentence([X|Rest],Idlen) :-
    upper first([X|Rest], [U|Rest]),
    write(U),
    name (U, LU), length (LU, L),
    (U = X, chkforpunct(U, Rest), !, write terms(Rest, L+Idlen);
     write(' '), write_terms(Rest, L+Idlen+1)
        write list inputs a PROLOG list and prints out a sentence like list.
         wrapped. Idlen is the starting position of the list in the output.
write list([X|Rest], Idlen) :-
    write(X),
    name (X, LU), length (LU, L),
   ( chkforpunct(X,Rest), write_terms(Rest, L+Idlen), !;
     write(' '), write terms(Rest, L+Idlen+1)).
%write_list(+List,+Idlen,-Idlenout)
% write_list prints out a sentence like list with wrapping if necessary.
    List is the list to be printed
    Idlen is the column position at start
    Idlemout is the column position at end
write_list([],Len,Len) :- !.
write list([X|Rest], Idlen, Idlenout) :-
    atomic(X), write(X),
    name(X,LU), length(LU,L),
    (L + Idlen > 74, nl, Idlen2 = 1, !;
     Idlen2 = L + Idlen, !
  (chkforpunct(X,Rest), write list(Rest,Idlen2,Idlenout), !;
    write(' '), write list(Rest, L+Idlen2+1, Idlenout), !
   is_list(X), write_list(X,Idlen,Idlen2), write_list(Rest,Idlen2,Idlenout).
upper_first([X|Rest], [U|Rest]):-
     name(X, [L|Z]),
 (is_alpha(L), Up is L - 32, !; Up = L),
 name(U,[Up[2]), !.
% write_terms/1 writes out a word followed by blank, except for punctuations.
write terms([]) :- !.
% case where X is end of sentence
write terms([X|Rest]) :-
   (X = '.'; X = ';'), % last word of sentence
   write(X), nl, !, write sentences(Rest), !.
% case where X is interior of sentence
write terms([X|Rest]) :-
     write(X),
     (chkforpunct(X,Rest), write_terms(Rest);
```

```
write(' '), write_terms(Rest)
% write_terms(List,Used): writes the terms in list and counts the number
        of columns used; starts new line if 75 columns have been used
write terms([],_) :- !.
% at end of list
write_terms([.], _) :- write('.'), nl,!.
write_terms((;], _) :- write(';'), nl,!.
% X is a punctuation, don't add to final count
write_terms([X|R],Used) :-
  (R = [], write(''), write(X), !;
    chkforpunct (X,R),
    write(X), write_terms(R,Used), !
% X is last word in sentence
write_terms([X,.], Used):-
   name (X, List), length (List, Len),
   Need is Len + 2,
   Total is Used + Need,
   (Total =< 75, write(' '), write(X), write(.);
    Total > 75, nl, write(' '), write(X), write(.)),
   nl, !.
% X is last word in sentence
write_terms([X,;], Used):-
   name(X, List), length(List, Len),
   Need is Len + 2,
   Total is Used + Need,
   (Total =< 75, write(' '), write(X), write(';');
    Total > 75, nl, write(' '), write(X), write(.)),
   nl, !.
% X is followed by ','
write_terms({X,','|Rest}, Used):-
   name (X, List), length (List, Len),
   Need is Len + 2,
   Total is Used + Need,
   (Total =< 75, write(' '), write(X), write(','),
    write_terms(Rest, Total);
    Total > 75, nl, write(' '), write(X), write(','),
    New is Need - 1, write terms (Rest, New)),
% writes blank + name of X, used is length of name+1
write terms([X|Rest], Used):-
   name(X, List), length(List, Len),
   Need is Len + 1,
   Total is Used + Need,
   (Total =< 75, write(' '), write(X), write_terms(Rest, Total);
    Total > 75, nl, write(' '), write(X), write terms(Rest, Len)),!.
write_terms(['X''s'|Rest], Used):-
   name(X, List), length(List, Len),
   Need is Len + 3.
   Total is Used + Need,
   (Total =< 75, write(' '), write(X), write("'s"),
    write_terms(Rest, Total);
    Total > 75, nl, write(X), write_terms(Rest, Len)),!.
% processes sentences in Infile; writes formats to Outfile
% sentences beginning with '%' are treated as comments
testsents(Infile,Outfile) :-
```

```
see (Infile), seen, see (Infile),
    tell(Outfile).
    readtests.
    see (Infile), seen, told.
% reads next sentence and processes it
readtests :-
    read in(X),
    (X = end_of_file, !;
     X = \{eoff, '.'\}, !;
     X = [''], !;
     X = ['%'], !, readtests; % don't process comments
     preprocess (X, Bs, Undef, Semlist, skip),
    ( Undef = [],
     dosent(X,Bs,Semlist,Fmt,Message,impression,W,chestxray,strict,0),
     write_sentence(X,1), write(Bs), nl,
     write(Fmt), nl;
     Undef \= [], write_sentence(X,1), write(Bs), nl, write(Undef), nl),
     readtests
                    % read next sentence
    ).
Reads in all sentences from input file and creates one list of all sentences
get_inputsents(Prevlist, Toklist) :-
     read_in(X),
     (X = end_of_file, Toklist = Prevlist, !;
      X = [eoff, '.'], Toklist = Prevlist, !;
      X = [''], Toklist = Prevlist, !;
      (last('',X), append(Toklist,[''],X), !;
                                                   %remove
       append (Prevlist, X, Newlist),
       get_inputsents(Newlist, Toklist)
      )).
*get sentence(+A,-B,-C)
* Gets next sentence from input list containing all sentences read in
Don't end a sentence if "." is preceded by a number and followed by
* a number and unit measure - 1.25 cm, 1.5 cm, .5 cm
t or is followed by a "." which is part of abbreviation
$ get_sentence(A,B,C) - A is list of all sentences in report.
                       - B is list containing one sentence
                       - C is remainder excluding B
* sgml tag for multi-word phrase containing '.' that is not end of sentence
get sentence(['<',phr|Tail],Sentence,LRest) :-
        enclosedPart (Tail, phr, Between, Rem), % Between beg. part of open phr and
close tag of phr
      append([sem,=,'"',Sem,'"'],MoreAttributes,Between), %Sem is value of sem
attribute
      (MoreAttributes = ['>'|Phrase], TargetList = Phrase, !;
       MoreAttributes = [t,=,'"'|TargetPlus], % Target terms plus end of phr append(TargetList,['"','>'|Phrase],TargetPlus), ! % t attribute followed
by actual phrase
      ١.
      Phrase = [W1|Rest],
      append (Phrase, SRest, Sentence),
      concat_atom(TargetList, Target),
      assert (phr (W1, Sem, Rest, Target)), % assert lex def according to input
        %Phrase = [W1|PRest],
        %abbrev(W1, [W1|PRest], Target, ),
        get_sentence(Rem, SRest, LRest), !.
```

```
% Ignore sentence starting with '%', get next sentence
get_sentence(['%','%'|Rest],Sent,Remainder) :-
     get_sentence(Rest,_,Rem),
     get_sentence(Rem, Sent, Remainder).
get_sentence([X,.,Y,Z|Rest],[X,.],[Y,Z|Rest]) :- % break up "140. 3+"
     number(X), number(Y), Z = '+', !. % Y belongs to '+' for new sentence
get_sentence([X,.,Y,Z|Rest],[N|SRest],LRest) :-
                                                       $ 1.5 cm
      number(X), number(Y),
      %(wdef(Z,unit,); Z = x),
      Z \= '+', % break up "140. 3+"
      1.
      name(X,D1), name(.,D2), name(Y,D3), name('E+00',D4),
      append([D1,D2,D3,D4],D), name(N,D), % put number together
      get sentence([Z[Rest],SRest,LRest).
% common abbrev
get_sentence([X,.|Rest],[X|SRest],LRest) :-
                                                 % abbrev ending in "."
% list of common abbreviations seen in reports should not end sentence
   member(X,[vs,dr,cm,mg]), get_sentence(Rest,SRest,LRest), !.
% list of start of names in reports should not end sentence
get_sentence([X,.|Rest],[X|SRest],LRest) :-
                                                 % abbrev ending in "."
   member(X, [ms, mr, mrs, dr, st]),
   skipname(Rest, Rest0),
                            % skip name part
   get_sentence(Rest0, SRest, LRest), !.
% more known abbreviations
get_sentence([W1|Rest],[Rep|SRest],LRest) :-
     abbrevchk([W1|Rest],_,Rem,Rep), % abbreviation
     get sentence (Rem, SRest, LRest), !.
* possible simple xml tag for new paragraph
get_sentence(['<',p,'/','>'|Rest],Sent,Rem) :- %skip paragraph marker
    get_sentence(Rest,Sent,Rem), !.
% xml tag for sentence '<s>'
get_sentence(['<',s,'>'|Tail],Sentence,Rest) :-
      enclosedPart (Tail, s, Sent, Rest),
       (last('.', Sent), Sentence = Sent, !; %already has '.'
      append(Sent,[.],Sentence)
                     %add '.'
       ), !.-
get_sentence([.|Rest],[.],Rest) :- !. %end of a sentence
get sentence([; |Rest],[;],Rest) :- !.
% interior of sentence
get_sentence([X|Rest],[X|SRest],LRest) :-
                       get_sentence(Rest, SRest, LRest).
get_sentence([],[],[]). % no more sentences
$ abbrevchk(+WordList,-AbList,-RemList,-Target) is true if an abbrev is prefix
    of WordList, RemList is suffix of WordList (excluding prefix),
    AbList is prefix consisting of abbreviation
    and Target is target form of abbreviation
abbrevchk([W1|Rest], AbList, RemList, Target) :-
     abbrev(W1,AbList,Target,Dom), % abbrev knowledge base indexed by 1st word append(AbList,Rem,[W1|Rest]), % remainder of abbrev. must be in sentence
     (Dom = general, !; % abbrev. applies to all domains
      domain(Thisrep), Dom = Thisrep, !; % abbrev. applies to this domain
      is list(Dom), member(Thisrep,Dom) % this domain in abbrev. list
     ( % add back '.' to sentence if it also signals end of sentence
       Rem = [], last('.', AbList), RemList = ['.'], ! *no more words
      ; % words that generally start a new sentence
```

```
Rem = [W2]_], last('.',AbList), member(W2,[his,her,he,she,the,this]),
         RemList = ['.'|Rem], !
         ; % don't add '.' back
       RemList = Rem
     ١.
% skipname(+Beglist,-Endlist): skips next word after "mr" or "st"
skipname([],[]) :-!.
skipname([_,'''',s|Rest],Rest):- !. % "Luke's"
skipname([0,''', |Rest],Rest):-!. % "O'Grady
skipname([ |Rest], Rest) :- !.
$get_section(+Toklist, -Sents, -Rest, -Section, -Printname, Addno)
% Toklist contains input list; 1st sentence should be a header;
* Sents are all sentences in section; Section is name of section
* Sentences at beg. of Toklist are ignored until a section header is found
get_section([T|Toklist], Sents, Rest, Section, Printname, Addno) :-
       % first sentence should be section header
      get_sentence([T|Toklist],Sentence,RToklist),
      (section_header(Sentence, Rsent, Section, Printname), % Sentence is a section
header
       append (Rsent, RToklist, RToklist2),
       get_sectionsents(RToklist2,Sents,Rest),
       (Addno = 0, !; % testing if input begins with section header
       Addno = 1, ! , sectno(Sectno), Newno is Sectno + 1,
       retractall(sectno(_)), assert(sectno(Newno))
       retractall(paragno(_)), assert(paragno(1)), %1st parag. of section
       retractall(sentno()), assert(sentno(0))
                                                   %1st sentence of parag.
       ; % 1st sentence is not a legitimate header - return []
        Section = []
       % get_section(RToklist,Sents,Rest,Section) % skip till find header
     ~), !.
get_section([],[],[],[],_,_).
get_sectionsents([],[],[]) :-!.
get sectionsents (Toklist, Slist, Rest) :-
     get_sentence(Toklist, Sentence, RToklist), % one sentence
     (\+ section_header(Sentence,_,_,), %more sentences in section
        get sectionsents (RToklist, RSents, Rest),
        append (Sentence, RSents, Slist)
       ; % the next section is a section header - return
      Rest = Toklist, Slist = (]).
section_header(S,RestS,'report clinical information item',
          'CLINICAL INFORMATION: .') :-
    (S = [clinical, information, ':', '.'], !, RestS = [];
     begsublist([clinical,information,':'],S,RestS), !;
     S = [clininfo,':','.'], RestS = {}, !;
     begsublist([clininfo,':'],S,RestS), !
   ).
section_header(S,RestS,'report impression item',
            'IMPRESSION:.') :-
   (S = [impression,':',.], RestS = [], !;
   begsublist([impression,':'],S,RestS), !
section_header(S,Rest,'report summary item','SUMMARY:.') :--
   S = [summary, ': | Rest].
```

```
section_header(S, RestS, 'report description item', 'DESCRIPTION:.') :-
   (S = [description,':',.], RestS = [], !;
   begsublist([description,':'],S,RestS), !
   ) .
section_header(S,Rest,'report diagnosis item','DISCHARGE DIAGNOSIS:.') :-
   (S = [discharge, diagnosis, ': '|Rest];
    S = [final, diagnosis, ': '| Rest];
    S = [principle, diagnosis, ':'|Rest]; S = [associated, diagnosis, ':'|Rest];
    S = [transfer,diagnosis,':'|Rest];
    S = [diagnosis,'(',es,')',':'|Rest];
    S = [diagnosis,: |Rest]
  ), !.
section_header(S,Rest,'report laboratory data item','LAB DATA:.') :-
    S = {laboratory, data, ': 'Rest}, !.
section_header(S,Rest,'report medications item','MEDICATIONS:.') :-
    S = [medications, ': '|Rest], !.
section_header(S,Rest,'report current medications item','MEDICATIONS:.') :-
    S = [current, medications, ': '|Rest], !.
section_header(S, Rest, 'report discharge medications item',
        'DISCHARGE MEDICATIONS:.') :-
    S = [discharge, medications, ': '[Rest], !.
section header(S, Rest, 'report discharge disposition item',
     'DISCHARGE DISPOSITION:.') :-
    S = [discharge, disposition, ': '|Rest], !.
section header(S, Rest, 'report medications on admission item',
     'MEDICATIONS: . ') :-
    S = [medications, on, admission, ': '|Rest], !.
section header(S, Rest, 'report medications on transfer iterm',
     'MEDICATIONS:.') :-
     S = [medications, on, transfer, ': '|Rest], !.
section_header(S,Rest,'report procedure item','PROCEDURE:.') :-
  (S = [operation, ': 'Rest]; S = [procedure, ': 'Rest]
  ), !.
section_header(S,Rest,'report indications for procedure item','INDICATIONS:.')
  (S = [indications, for, procedure, ': '|Rest]; S =
[indications, for, operation, ': ' | Rest]
 ),
  1.
section_header(S,Rest,'report preoperative diagnosis item','PREOP DIAGNOSIS:.')
   S = [preoperative, diagnosis, ': '|Rest], !.
section_header(S,Rest,'report admitting diagnosis item','ADMITTING
DIAGNOSIS: . '):-
   S = [admitting, diagnosis, ': '|Rest], !.
section_header(S,Rest,'report postoperative diagnosis item','DIAGNOSIS:.') :-
   S = [postoperative, diagnosis, ': '[Rest], !.
section header(S, Rest, 'report physical examination item',
        'PHYSICAL EXAM: . ') :-
   S = [physical, examination, ': 'Rest], !.
section_header(S,Rest,'report chief complaint item','CHIEF COMPLAINT:.') :-
  S = [chief,complaint,':'|Rest], !.
section_header(S,Rest,'report hospital course item','HOSPITAL COURSE:.') :-
  S = [hospital, course, ': 'Rest], !.
```

```
section header(S, Rest, 'report allergy item', 'ALLERGIES:.') :-
   S = [allergies, ': '[Rest], !.
section_header(S,Rest,'report follow up item','FOLLOW UP:.') :-
   S = [follow,up,':'|Rest], !.
section_header(S,Rest,'report findings item','FINDINGS:.') :-
   S = [findings,':'|Rest], !.
section_header(S,Rest,'report indications and findings item','FINDINGS:.') :-
   S = [indications, and, findings, ': '|Rest], !.
section_header(S,Rest,'report indications and findings item','INDICATIONS:.') :-
   S = [indications, ': '|Rest], !.
section_header(S,Rest,'report provisional diagnosis item','PRELIM DIAGNOSIS:.')
   S = [provisional, diagnosis, ': '[Rest], !.
section_header(S,Rest,'report review of systems item','REVIEW OF SYSTEMS:.') :-
   S = [review, of, systems, ':'|Rest], !.
section_header(S,Rest,'report past history item','PAST MEDICAL HISTORY:.') :-
   S = [past, history, section, ': '[Rest], !.
section_header(S,Rest,'report past history item','PAST MEDICAL HISTORY:.') :-
   S = [past, medical, history, ': 'Rest], !.
section_header(S,Rest,'report social history item','SOCIAL HISTORY:.') :-
   S = [social, history, ': '| Rest], !.
section_header(S,Rest,'report past history item','PAST MEDICAL HISTORY:.') :-
 . S = [history,':'|Rest], !.
section_header(S,Rest,'report past history item','PAST MEDICAL HISTORY:.') :-
   S = [brief, history, ':'|Rest], !.
section_header(S,Rest,'report history of present illness item',
         'HISTORY OF PRESENT ILLNESS:.') :-
   S = [history, of, present, illness, ': '|Rest], !.
section_header(S,Rest,'report history of present illness item';
         'HISTORY OF PRESENT ILLNESS:.') :-
   S = {history, of, the, present, illness, ':' | Rest}, !.
section_header(S,Rest,'report specimen item','SPECIMEN') :-
   S = [specimen|Rest], !.
* sentence consists of id number only or "." only.
isidentifier([X,.]) :-
        integer (X).
isidentifier([X,;]) :-
        integer(X).
isidentifier([.]) :- !. % sentence consists only of .
isidentifier(['.','<eos>']) :- !.
isidentifier(['<',p,'/','>']) :- % paragraph marker sentence - update no.
       paragno(N),
       retractall(paragno(_)),
       Newno is N + 1,
       assert (paragno (Newno)),
       retractall(sentno(_)),
       assert (sentno(0)).
% skipsentence is true, if sentence should be ignored.
% Skip sentences containing family info
skipsentence([X|_]) :-
   foundword(X, family), !.
skipsentence([X|]) :-
   foundword(X, insurance), !.
% This occurs if sentence contains
```

```
% a sequence in skips database and sentence also contains findings.
skipsentence([X|Rest], Semlist, Error) :-
                     % X is the beg. of subseq. in skip database
   skips([X|Sseq]),
   prefix([X|Rest],[X|Sseq]), % sentence contains subseq.
   (subtype(_,Semlist), % sentence contains information to be extracted
   Error = no; % don't try to segment
   Error = yes), !. % treat sentence as error and try to segment.
skipsentence([ |Rest], Semlist, Error) :-
   skipsentence (Rest, Semlist, Error).
% findingseg(+S,-Fseg,-Begseg): partitions sentence
        S is the sentence; Begseg is the segment preceding the
          modifiers of the finding; Fseg is the segment of S starting
ž
          with the leftmost modifier of the finding and consists of the
¥
          remaining sentence.
findingseg(S,Fseg,Begseg) :-
   partition(S, Begpart, Restpart),
    (Begpart = [], Begseg = [];
    Restpart = [], Fseg = [], Begseg = S;
    right1stmod(Begpart, Begseg, Modseg)),
    append (Modseg, Restpart, Fseg).
findingseg(_,[],_) :- !.
actionfindingseg(S,Fseg,Begseg):-
      partition(S, Begpart, Restpart),
    (Begpart = [], Begseg = [];
     Restpart = [], Fseg = [], Begseg = S;
      reverse (Begpart, ReversedBefore),
          findsubstance (ReversedBefore, Rest),
          append (Substancepart, Rest, ReversedBefore).
          reverse (Substancepart, Leftpart),
        reverse (Rest, Begseg),
      append(Leftpart, Restpart, Fseg)).
actionfindingseg(_,[],_) :- !.
findsubstance([],[]):- !.
findsubstance([X|Rest],Rest):-
      substance(_,[X],[]),!.
findsubstance([X Rest1], Rest):-
      findsubstance (Rest1, Rest).
% partition(+S,-Begpart,-Restpart): partitions sentence
        S is initial
% partition(+S,-Begpart,-Restpart): partitions sentence
        S is initial sentence; Begpart is part of sentence before the
          finding; Restpart is the rest of the sentence and starts with
*
          the finding. If there are 2 consecutive findings
*
          the 1st one is considered a modifier
partition([],[],[]) :- !.
partition([X|Rest],[X|Begpart],Restpart) :-
    not(isfinding(X)), !, partition(Rest, Begpart, Restpart).
partition([X,Y|Rest],[X],[Y|Rest]) :-
    isfinding(X), isfinding(Y), !.
partition([X|Rest],[],[X|Rest]) :-
    isfinding(X), !.
% isfinding(+X): is true if X is a word or phrase whose semantic class
        is a finding or subtype of finding.
```

```
isfinding(X) :-
     foundword(X,Sem), % semantic class of word
                        % is class a type of finding, recommend, or technique
     subtype( , [Sem]).
% semantic class which are types of relevant information
subtype (finding, Sem) :-
     intersect(Sem, [attach, createbond, breakbond, activate,
      inactivate, substitute, transcribe, express, promote,
      signal]).
% there is only one type of technique class
subtype(technique,Sem) :-
     member (technique, Sem).
subtype(time, Sem) :-
     intersect (Sem, [status, sstatus, change, tmper, vstatus]).
findinginlist(Sem) :-
    intersect(Sem, (attach, createbond, breakbond, activate,
      inactivate, substitute, transcribe, express, promote,
      signal]).
% chkforpunct(+W, +Rest): is true if there should be no space after word W
chkforpunct(W,_) :- member(W,['/','<','>','-','"','[',']',
               `'{';'}','<u>_</u>','+','=','|','\']), !.
% nothing left to write.
chkforpunct(W,[]) :-!.
% is true if there should be no space before word after current word
chkforpunct(_,[W|_]) :-
   ispunct(W).
% ispunct(+W) is true if W is a punctuation for sentence print out
                                                         # $ ^ & *
% The following characters are not treated as punct: ~ `
'{','}','(',')','_','+','=','|','\','\*','@'}).
% right1stmod(List, Firstpart, Modpart): Modpart begins with the first
    word in List which is a modifier; Firstpart are the preceding words
right1stmod([],[],[]) :- !.
% X is a modifier or finding; Beginning part is empty
rightlstmod([X|Rest],[],[X|Rest]) :-
   foundword (X, Sem, Target),
   (modifier(Sem); Sem = p, Target = [ ,conn); subtype(_,[Sem])), !.
% X is not a modifier or finding
right1stmod([X]Rest],[X]Firstpart],Modpart) :-
   right1stmod(Rest, Firstpart, Modpart).
% frame(Frame, Type, Value, Mods): creates a list Frame, whose 1st
        element is Type, 2nd element is Value, and 3rd is a list of
ş.
        modifier frames or is emtpy
% Case where modifier list is empty; Value should be atom except for
% certain types;
frame([Type, Value], Type, Value, X) :-
    (X = []; X = [[]]),
    atom(Value), !.
% Special cases where value of type should be a list
frame([Type, [H|R]], Type, [H|R], X) :-
       (X = []; X = [[]]),
       oklist(Type), !.
% Modifier list is merged with list consisting of Type and Value
frame (Frame, Type, Value, Mods) :-
     atom(Value),
     append([Type, Value], Mods, Frame), !.
```

```
frame (Frame, Type, [H|R], Mods):-
      is list(R),
      append(R, Mods, NewMods),
      append([Type, H], NewMods, Frame), !.
 % Components of Frame
 frame([Type, Value | Mods], Type, Value, Mods) :- !.
 % Value of Type should not be a list; first element of value is real value
 frame([Type, H, Rest], Type, [H|Rest], []) :- !.
 % Special cases where value of type should be a list
%frame([Type, [H|R]], Type, [H|R], []) :- %repeated from rule above
    oklist(Type), !.
 % Value of Type should not be a list; first element of value is real value
 frame (Frame, Type, [H|Rest], Mods) :-
    mergemods (Rest, Mods, NewMods),
     append ([Type, H], NewMods, Frame).
 % mergemodinf(-F,+Frame,+Mods): Frame is a type-value-mod frame; Mods
    is an additional set of modifiers for Frame; mergemodinf adds Mods
    to Frame, resulting in F.
mergemodinf([],[],_):-!.
mergemodinf(F,[rel,X|Rest],Modrel):-
         mergemodinf(F1, Rest, Modrel),
         append([rel,X],F1,F),!.
. mergemodinf(F,[F1,X|Modfin],Modrel):-
         atom(F1), mergemods(Modrel, Modfin, Mod),
         append([F1,X],Mod,F),!.
 mergemodinf(F,[H|R],Modrel):-
       mergemodinf(F1,H,Modrel),
         mergemodinf (F2, R, Modrel),
         append([F1],F2,F).
% addmodstof(+Args,+Mods,-NewArgs) is true if Args is a list of formats,
% Mods is a list of modifiers and NewArgs is a list of formats where Mods
 % has been added to modifier list of that format
 addmodstof([],_,[]) :- !. % no more formats
 addmodstof([Format1|Rest], Mods, [F1|NewRest]) :-
        mergemodinf(F1, Format1, Mods), % merge modifiers into 1st format
        addmodstof(Rest, Mods, NewRest), !. %add modifier to remaining
 % oklist(+Type): is true if Type can have a list as its value
oklist (unitval).
oklist (age).
oklist (measure).
oklist(prev timeunit).
oklist (future_exam).
% mergemods(+Mods1,+Mods2,-Mod): Mods1 and Mods2 are a list of modifier lists
         Mod is the merged list; some elements of Mods1 and Mods2 may be
 *
         empty
mergemods([],M,M) :- !.
mergemods (M, [], M).
mergemods (Mods1, Mods2, Mod) :-
         delete(Mods1,[],M1),
         delete (Mods2, [], M2),
         append (M1, M2, Mod).
 $ addmod(+Mod,+Modlist,-NewMod): NewMod is formed by including
        Mod into Modlist
addmod([], Mod, Mod) :-!.
```

```
addmod(Mod,[],[Mod]) :- !.
addmod (Mod, Modlist, NewMod) :-
   append([Mod], Modlist, NewMod).
% modlist(+ListofMods,-Mods): ListofMods is a list consisting of
    individual modifier frames, some of which may be empty
    Mods is formed as a list of non-empty modifiers
modlist([],[]) :- !.
% ignore a modifier which is an empty list
modlist([[]|R],Mods) :-
    modlist(R, Mods), !.
modlist([[H|R1]|R2],Mods) :-
    atom(H), !,
    modlist (R2, Rmods),
    addmod([H|R1], Rmods, Mods).
modlist([[H|R1]|R2],Mods) :-
    is_list(H), !, % is first element is a list
    modlist (R2, Rmods),
    mergemods([H|R1],Rmods,Mods).
$bpframe: creates from for sequences of bodyloc/region/position
bpframe(F,[],_,F,[]):- !. % only 1 bodyloc
bpframe(F,[],Type,Bp1,Bp2) :- % no conj relation but more than 1 bodyloc
        frame(Bp1,Bp1Type,Bp1Val,Bp1Mods), %contents of Bp1 frame
        frame (Bp2, Bp2Type, Bp2Val, Bp2Mods), %contents of Bp2 frame
        ( (Bp1Type = region; Bp1Type = position),
         Bp2Type = bodyloc, % 'left lung', 'area of lung'
         mergemods (Bp1Mods, Bp2Mods, BpMods), *new region modifier
         frame (NewBp2Mods, Bp1Type, Bp1Val, BpMods), %new Bp1 frame w new mod
         BplType = bodyloc, Bp2Type = bodyloc, Type = main, %Bp2 is main
         mergemods (Bp1Mods, Bp2Mods, BpMods), *new bodyloc modifier
         frame (NewBp2Mods, Bp1Type, Bp1Val, BpMods), % 'joint of shoulder'
                                                  % main bp frame is shoulder
         frame(F, Bp2Type, Bp2Val, [NewBp2Mods])
         mergemods (BplMods, Bp2Mods, BpMods),
         frame (NewBp1Mods, Bp2Type, Bp2Val, BpMods), % 'shoulder joint'
         frame(F,BplType,BplVal,[NewBplMods])
                                                   % main bp frame is shoulder
bpframe(F,Rel,_,Bp1,Bp2) :- % no conj relation but more than 1 bodyloc
        Rel = [rel,Conj|_], Bp2 \= [],
        mergemods([Bp1],[Bp2],Conjargs),
        frame(F,rel,Conj,Conjargs).
getrelation(R,F1,F2,F) :-
        (F2 = [],
            (F1 = [rel,Conj1|Rest1], R = [rel,Conj],
                                   (Conjl = ','; Conjl = or; Conjl = and),
                                   (Conj = ','; Conj = or; Conj = and);
             Rest1 = \{F1\},
            (F2 = [rel,Conj2|Rest2],
                                   (Conj2 = ','; Conj2 = or; Conj2 = and);
             Rest2 = [F2]),
           %splice([R,Rest1,Rest2],F);
            append([R,Rest1,Rest2],F);
          F2 = [], F = F1].
```

uptotal : addstotal(X),
 X =< 50,
 NewX is X + 1,
 retractall(addstotal(X)),
 assert(addstotal(NewX)), !.</pre>

Appendix **F**

```
$save{'a'}='AAAC';
 $save{'b'}='AAAG';
 $save{'c'}='AAAT';
 $save{'d'}='AACC';
 Ssave{'e'}='AACG';
 $save{'f'}='AACT';
 $save{'g'}='AAGC';
 $save{'h'}='AAGG';
 $save{'i'}='AAGT';
 $save{'j'}='AATC';
 $save{'k'}='AATG';
$save{'1'}='AATT';
 $save{'m'} = 'ACAC';
 $save{'n'}='ACAG';
 $save{'o'}='ACAT';
 $save{'p'}='ACCC';
 $save{ 'q' }= 'ACCG';
 $save{'r'}='ACCT';
 $save{'s'}='ACGC';
 $sa 'e{'t'}='ACGG';
 $save{'u'}='ACGT';
 $save{'v'}='ACTC';
 $save{'w'}='ACTG';
 $save{'x'}='ACTT';
 $save{'y'}='AGAG';
 $save{'z'}='AGAT';
 $save{'0'}='AGCC';
 $save{'1'}='AGCG';
 $save{'2'}='AGCT';
 $save{'3'}='AGGC';
 $save{'4'}='AGGG';
 $save{'5'}='AGGT';
 $save{'6'}='AGTC';
 $save{ '7'}='AGTG';
 $save{'8'}='AGTT';
 $save{'9'}='ATAT';
 $save{' '}='ATCC';
 $save{'}'}='ATCC';
 $save{'{'}}='ATCC';
 $save{';'}='ATCC';
 $save{':'}='ATCC';
 $save{'"'}='ATCC';
 $save{'\''}='ATTC';
 $save{'?'}='ATCC';
 $save{'!'}='ATCC';
 $save{'#'}='CCCG';
 $save{'$'}='CCCT';
 $save{'^'}='CCGG';
 $save{'&'}='CCGT';
 $save{'*'}='CCTG';
 $save{'('}='ATCC';
 $save{')'}='ATCC';
```

NXQ2:257372.1

```
$save{'_'}='CGCT';
$save{'-'}='ATCC';
$save{'+'}='CGGT';
$save{'='}='CGTG';
$save{'}'}='CGTT';
$save{'{'}='CTCT';
$save{','}='ATCC';
$save{'.'}='ATCC';
$save{'|'}='CTTG';
$save{'%'}='CTTT';
$save{'/'}='ATCC';
$save{'\\'}='GGTT'; .
$save{'@'}='GTGT';
$save{"\n"}='ATCC';
$save{'<'}='GTTT';
$save{'>'}='GTTT';
$save{'~'}='GTTT';
```



Appendix F

```
#!/usr/bin/perl
#Scan.pl : Scans blast output
#Author: Michael Krauthammer
#Copyright: c.1999, Columbia University
#Variables
#blast input/file
$input file="genebank.result";
#program output
$output_file="match.txt";
#open datastream for file which contains blast output
   open (INPUT,'/storage/psi-blast/MarkIt/programs/markIt.result');
while ($line=<INPUT>) {
   if ($line=-/\>gi\|(\d*) (.*)\,(.*)\,(.*)/){
   $target=$4;
  $qi =$1;
   $semantic_class=$3;
   }
   if(sline=-/Length = (.*)/){
   $lengthI=$1;
   if \{$line=~/Identities \= (\d*)\//){
   $length_actual=$1
   if ($line=~/Query: (\d*)/){
   $start=$1;
#print if Subj 1, sometimes match 2 or 3 line long
    if ($line=-/Sbjct: 1 /) {
   if (($length_actual/$lengthI) > .9){
$target,"|-",$start,"|",$start+$lengthI,"|",$semantic_class,"|",$gi,"\n";
}
```

Appendix G

```
#!/usr/bin/perl
   #nucleotide text_parser.pl
#Author: Michael Krauthammer, c.1999 Columbia University
   open (INPUT, $ARGV[0]);
   #read uncoded input text line by line (chop it)
   $all='';
   while ($line=<INPUT>) {
              $all=$all.$line;
   open (INPUTII, '/storage/psi-blast/MarkIt/programs/markItII.result');
   open (OUTPUT, '>result.txt');
   #first part: check matches, store positions
   while ($line=<INPUTII>) {
 (Sname, start, end, semantic class, gi) = sline = -/(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|(.*)\|
   #divide by 4 (4 letter code)
   $start=($start-1)/4;
   $end=($end-1)/4;
   #get substring
    if ($start != 0){
    $letters=substr($all,$start-1,$end-$start+3)."|";
    } else {
    $letters = ' '.substr($all,0,$end+2)."|";
    ($letter beginning)=$letters=-/(^.)/;
    $letter end=substr($all,$end,1);
    $letter endII=substr($all,$end,2);
    #ignore matches that are in the MIDDLE of sentences, allow plurals
    $letter beginning=~tr/[A-Z]/{a-z}/;
    $letter end=~tr/[A-Z]/[a-z]/;
    if ((!($letter_beginning=~/[a-z]/)) && ((!($letter_end=~/[a-z]/)) ||
    ($letter endII=~/s /))){
    #make sure only the first occurence is stored at this position
            if ($save{$start}==''){
            $save{$start}=$end.'|'.$semantic class.'|'.$gi;
                            foreach $key(keys(%save)){
            ($end_key) = $save {$key} = -/^(.*) \ \ /;
            if ($end key>$end) {
                     if ($key<$start){
                            $save{$start}='null',
            }
```

```
#second part: print out marked up document
sort(%save);
for ($i=0;$i<length($all);$i++){
    if ((!$save{$i}=='null') && ($save{$i}=-/./)){
        ($end.$semantic_class)=$save{$i}=-/.*)\|(.*)\|/;
        print OUTPUT '<phr="'.$semantic_class,'">';
        $store=substr($all,$i,$end-$i);
        print OUTPUT "</phr>";
        $i=$end-1;
        } else {
        $store=substr($all,$i,1);
        print OUTPUT $store;
    }
}
```

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-2427	-255		-2478	-255		-2478	-255		-2615	-255		-786	-255		-2740	-255		-2760	-255		.2791	-255		.2729	-255		-2751	-255		-2750	-255		-2756	-255		-2770	-255		-2703	-255		-2770	-255
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-2145	7.2		-2197	27		-2197	27		-2334	27		-2459	27		-525	27		-859	27		-128	27		-2447	27		-2300	72		240	27		-2474	27		655	27		-139	27		٣	27
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779	-335		9.2	-335		-2558	-335		-2696	-335		-2145	-335		-1071	-335		-2840	-335		- 904	-335		-174	-335		837	-335		269	-335		-288	-335		-372	-335		389	-335		493	-335
802	- 73		-243	-73		-2296	-73		-400	- 73		1408	-73		-72	-73		167	73		511	-73		-406	-73		-2317	-73		- 94	-73		-539	-73		-530	- 73		876	-73		-377	-73
1358	41		-235	41		-2183	47		-782	41		-706	41		5.8	41		-487	41		-2495	41		1035	41		190	41		-2455	41		1371	47		-518	4		1427	41		805	41
60	-164		-2388	-164		-2388	-164		-2525	-164		-165	-164		-2273	-164		-84	-164		120	-164		1034	-164		975	-164		443	-164		-274	-164		-63	-164		-2612	-164		-658	-164
-2849	-677		516	-617		-2900	-617		-1622	-677		543	-677		-3162	-677		1292	-677		-479	-677		-244	-677		-3173	-677		21	-677		358	-617		206	-677		-3125	-677		-1530	-611
77	-130		719	-130		1493	-130		1387	-130		812	-130		1116	-130		640	-130		4 94	-130		-495	-130		-928	-130		95	-130		875	-130		163	-130		476	-130		514	-130
-840	438	•	-1052	438	•	-300	438	•	-617	438	•	-477	438	٠	- 569	438	٠	143	438	•	145	438	•	-500	438	•	479	438	*	-614	438	•	-281	438	•	584	438	•	1032	438	*	-806	438
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585	-116	267	585	- 98	267	585	- 98	275	585	-97	307	•	٠
372	-3689	54	372	.3923	54	372	-3923	62	372	-3946	94	*	•
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-352	-732	-670	-352	-732	-670	-352	-732	-663	-352	-732	-630	•	•
-178	-3417	-496	-178	-7215	-496	-178	-5577	-489	-178	-3923	-456	٠	•
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		616	-178	-352	. 36		585	.635	438	-130	-677	-164	41	-73	-335	.54	27	-12	-255	-97
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		919	-178	-355	- 36		585	-635	438	-130	-617	-164	41	٠.	-335	.54	27	-12	-255	-97
	•	10434	-5577	-732	-1329	•	-105	•	•											
•	639	146	237	-154	361	•	1779	-1139	529	262	-2880	-1519	397	569	-320	-452	-2108	638	-2555	1020
	206	979	.178	. 352	-36	372	585	-635	438	.130	-677	-164	\$.73	:335	.54	27	-12	-255	-97
	•	10404	-6255	.732	-1329	•	-164	•	•											
0		-1331	119	-690	-582	.1437	-807	420	930	-2440	1026	-717	1162	1,1	157	- 926	-602	455	1032	1056
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. •	206	979	.178	.352	-36		585	-635	438	-130	-677	.164	7		13.5	.54	27	-17	-255	. 97
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/10302

IPC(7) US CL	SSIFICATION OF SUBJECT MATTER : G01N 31/00; G06F 15/00, 17/00 : 702/27; 706/45, 47; 712/200 o International Patent Classification (IPC) or to both	national cl	assification and IPC								
B. FIEI	DS SEARCHED										
	ocumentation searched (classification system followed 102/27; 706/45, 47; 712/200	by classification symbols)									
Documentati	ion searched other than minimum documentation to the	e extent th	nat such documents are include	d in the fields searched							
	ata base consulted during the international search (nationalise on the continuation Sheet	me of data	base and, where practicable, s	search terms used)							
C. DOC	UMENTS CONSIDERED TO BE RELEVANT										
Category *	Citation of document, with indication, where a	ppropriate	, of the relevant passages	Relevant to claim No.							
Y	YUAN et al. Towards detection of orthologues in s 1998, Vol. 14, No. 3, pages 285-289, see entire do		atabases. Bioinformatics.	1-32							
Y	BAILEY, JR. et al. Analysis of EST-driven gene a Genome Research. 1998, Vol. 8, pages 362-376, se	nnotation e entire de	in human genomic sequence.	1-32							
Y	SONNHAMMER et al. Pfam: A comprehensive da based on seed alignments. Proteins: Structure Fund pages 405-420, see entire document.			1-32							
	r documents are listed in the continuation of Box C.		See patent family annex.								
"A" documen	pecial categories of cited documents: 1 defining the general state of the art which is not considered to be	*T*	later document published after the inte date and not in conflict with the applic principle or theory underlying the inve	cation but cited to understand the							
	ular relevance opplication or patent published on or after the international filing date	-x-	document of particular relevance; the considered novel or cannot be conside when the document is taken alone								
	t which may throw doubts on priority claim(s) or which is cited to the publication date of another citation or other special reason (as	- Y-	document of particular relevance; the considered to involve an inventive ste								
	of referring to an oral disclosure, use, exhibition or other means		combined with one or more other such being obvious to a person skilled in th	documents, such combination							
"P" document priority	t published prior to the international filing date but later than the date claimed	-&*	document member of the same patent	family							
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	shington, D.C. 20231 o. (703) 305-3230	Telepho	ne No. (703) 308-0196								

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT	International application No.
	PCT/US00/10302
Continuation of B. FIELDS SEARCHED Item 3: STN Commercial Database (B SciSearch, Biotechds, Caplus)	liosis, Medline, Embase, Embal,
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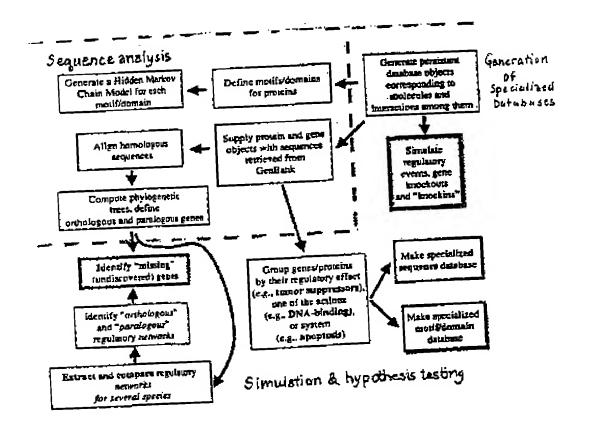


FIGURE 1

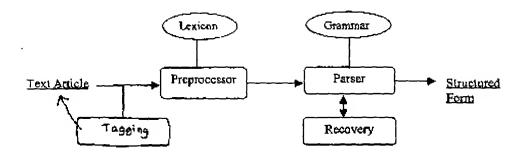


Figure 2

BNSDOCID <WO__0063687A1TI_>

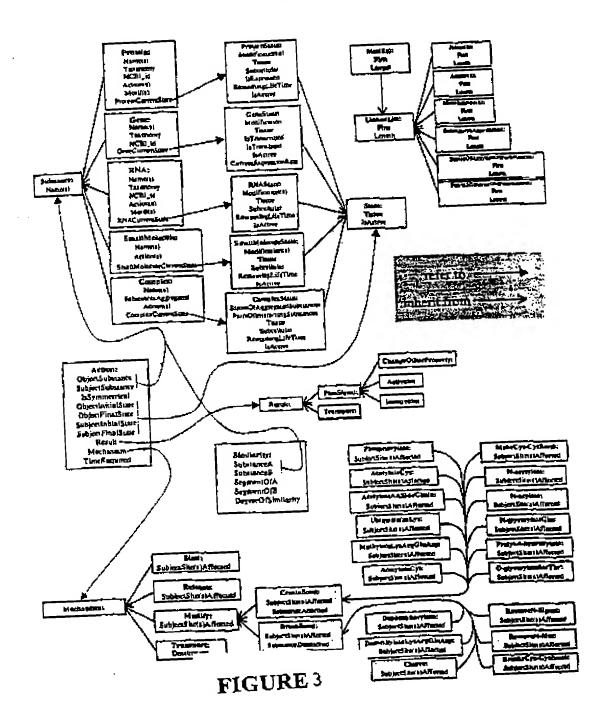


FIGURE 4

bd-sl./ bd / bc-ss/ cmi-9/ Bux / Bix / Bix / Bix / Rix / NGF1-8/ NIG / Nahl / Nur?? / Nurl / Norl / Norl / Ext / giccio-1/ Neglyana / CNTF / ick / tyb / ZAP-70 / raf / raf / MAP / protein kinase C / PEC / phosphotos calcinents / NG-AT / ARI / IA-3 / Raf-1 / Bcl-2 / Intertestion / IL-1 / EL-1 / CD-2 / cytokine / IGF-1 / CD-9 / Apo-1 / Rip / YAF1 / PADD / PAP-1 / TWFR / TRAP1 / TRAP1 / TRAP1 / TRADD / BLAP1 / HARP2 / CD-0 / CD-9 / CD-2 / CD-1 / TCR / Bcl-2 / Nes-1 / Nes-1 / NR-13 / BRAP1 / EMTW-EL / ELBYSK / NSK / Mch-2 / CPF-2 / ICE / FLICE / Nes-1 / TS / Mch-3 / MCh-1 / KCE-1 / mch-1 / INAMI / copuse / MACH1 / Mch-2 / Tyb / NSK / NSK / NSK / MCK-2 / MCK-

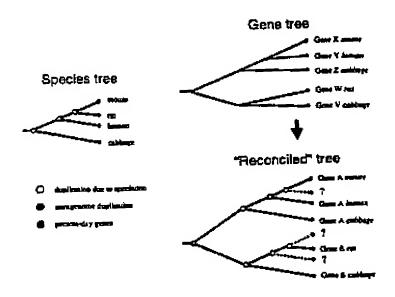


FIGURE 5

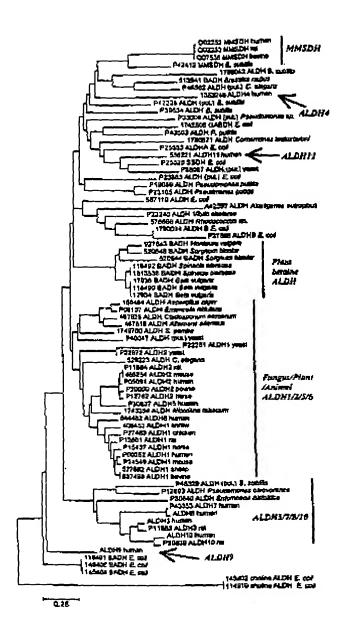


FIGURE 6

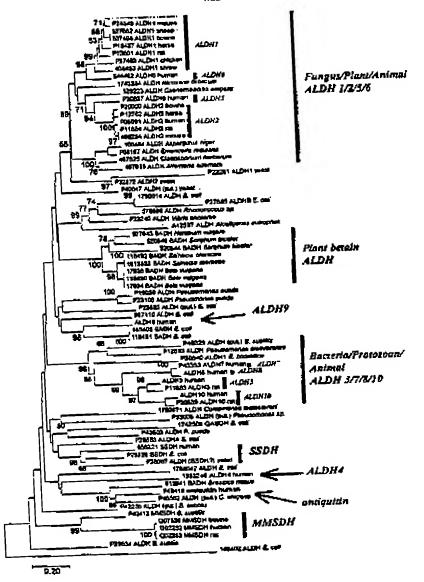


FIGURE ?

FIGURE 8

Start with Start with Start with a single Biological system a gene family a single gene Reconstruct a "network" of interacting genes and proteins Identify a set of key domains and motifs Search for related motifs in databases of known organisms Identify members of multigene families Compute phylogenetic trees Paralogous navorks Identify clusters of paralogous genes, identify paralogous and onholbgots Henvorks Mining receipt Parelogous networks in human أعامهم للراطرين Compare regulatory schemes, identify genes that are known in one but missing in another system.

Find the genes using experimental techniques.

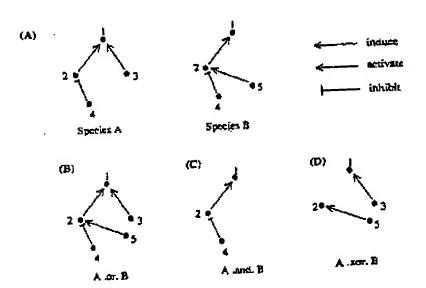


FIGURE 9

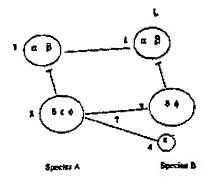


FIGURE 10

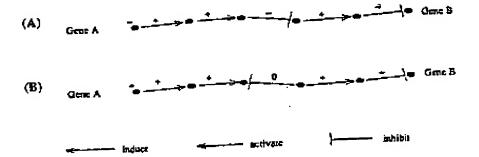


FIGURE II

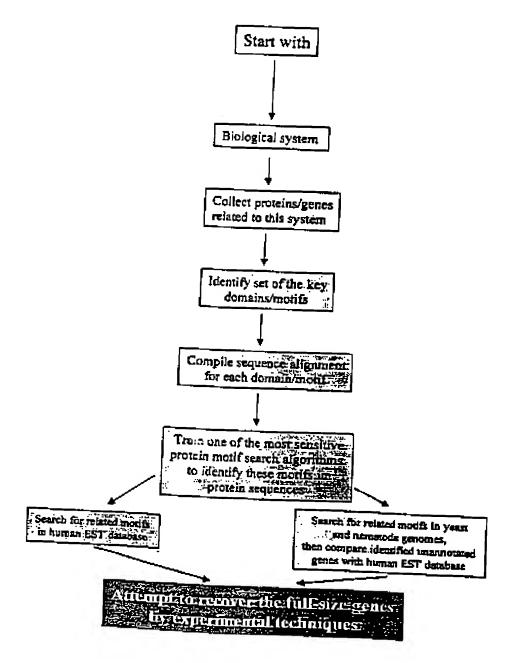


FIGURE 12.

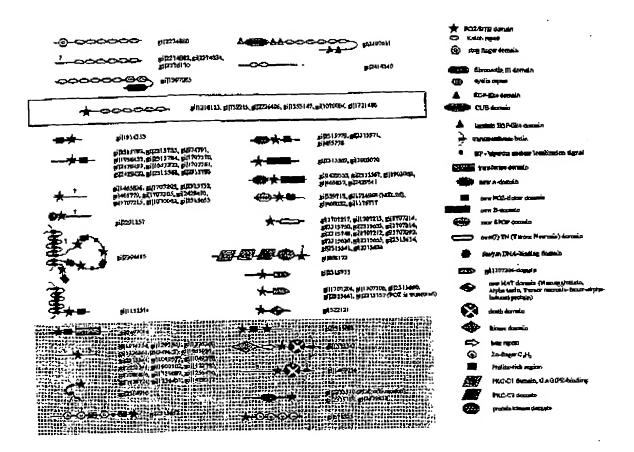


Figure 13

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Figure 14A

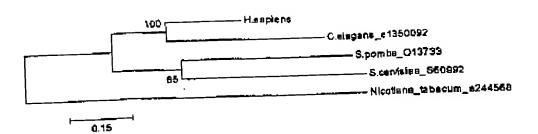


Figure 14B

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ORIGIN
        1 caqceqA8GC AmgcA8888t tetteragga getgaqcaag agootggacg catteretga
       61 ggayttotgt oggoacaagg tgotgoocca gotgotgaco goottogagt toggoaatgo
      121 tagggoogtt gtoutcaege contettera ggtaggoaag ttoutgageg etgaggagta
      181 teagengang atentecets togitogican gatotteten temacipace godecatges
      241 catcogeste ctgcsgcaga tggsgcagtt catcomptee cttgacgage caacagteaa
      301 cacceagate theococacy toptacatey effectigae accuaecety coatcagge
      361 gengacygic magiciatge typicetgge decamagety amegnyges accidentist
      421 ggagetgatg aagcacttig cacggotaca ggccaaggat gaacagggee ceateegetg
      481 cascacceCA gtctgcctpg gcaaaategg cicctacctc agigctsgca ccagacacag
      54) ggtoettace tetgeettea geegageeae tagggaeeeg titgeaeegt eeegggittge
      601 gggtgtcctg ggctttgctg.ccacccacaa cctctactca atquacqact gtgcccagaa
      663 gatcotgcct gigatetgeg gitteetgi agatooigag asatoogige gagaceagee
      721 ottobaggem witteggaget teetgteeaa attggagtet gtgteggagg accegaecea
      781 gctggaggaa gtggagsagg atgtccatgs agsctccags cetggsatgg gaggagssg
      841 agetaget99 90agget999 egtgaceg99 gteteeteat teaceteea getgateegt
     901 topeaccess coertgood ascapasace secattood sesenteese geetgasggs
      961 gttoctgece cagecectat centgttest gecacectta caacetcagg coartgggag
     1021 acycaggagg aggacaagga cacagcagag gacagcagca ctyctgacag atgggacgac
     1081 gaagactggg Gragectgga geaggaggee gagtetgtge tggcccagea ggacgaetgg
     1161 ageaccagag gcommagtag controller cannot accompace actualization
     1201 sastcoocky detecatety gameagetag gameetagg getectagga acaggactag
     1261 caggagecaa geteccagga gecacetyet gacggtacae ggotggoray cgagtataac
     1321 tggggtggcc cagagtccag cgacaagggc gattetteg ctaecetgte tgcacqtccc
     1381 agencerace coarrecage etettogget gangacaset goggaggeet ogsgaetgae
     1441 agtogacagg teaaggetge getggeeegg aagaagegeg aggagegeg geggagatg
     1501 gaggectaato gogoogagag gaaggtgooz, agggeeceat gaagetggga geseggaage
     156) togactgest cottocopy geoettecam garagaga pacagoosa cagatgtatt
     1621 tattgtacks scottgtgsg beeggeegee cagesagger atotexcgtg tacateates
     1681 gagccacat easttotett toacaaaaa aassasaa aassasa
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Figure 14C

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121	Q	T	ν	K	5	N	L	L	L	A	P	K	L	N	E	А	N	L	Ŋ	γ	E	.L.	M.	Х	H	F.	Α	R	L	Q	
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241	E	К	A	X	R	S	F	L	5	ĸ	L	E	S	٧	5	E	D	P	7	Q	Ŀ	E	E	٧	E	К	Ð	¥	H	A	
271	A	5	8	P	Ģ	М	Ģ	G	A	A	A	8	IJ	A	G	И	Α														

Figure 14 D

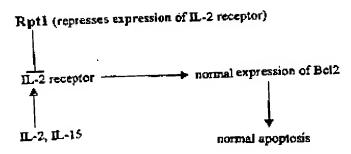
>sp|P15533|RPT1_MOUSE DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR (J03776) rpt-1r [Mus musculus] Length = 353

Score = 92.0 bits (237), Expect = 6e-20

Homology covers ring finger, B-box and the beginning of coiled coil domain in the CLL ring finger protein

Figure 15

Activated CD4+ T-cells



When rpt1 is knocked out:

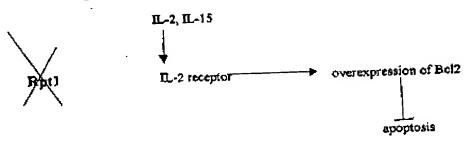


Figure 16

TALKSTH 2.0.8 [Jan-05-1989]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. BchBISer, Jinghul Sheng, Eheng Shang, Webb Miller, and David J. Lipman (1997), "Gapped SLAS" and PSI-SLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. Query= q1/2137498|Med3m (205 letterm) gb;aA278224!AA278884 #877005.21 HCI_CGAP_GCG1 Homo sepiene cDNA clone IMAGE:7DE520 5* ELOGIAT TO TRIGITERIST GITERIET MEX-INTERACTING TRANSCRIPTIONAL ALPRESSOR. , Congth # 430 Score = 209 bits (526), Expert = 1e-63 Identities = 104/124 (836), Positives = 118/124 (926), Gaps = 1/124 (98) frame = +2 Quety: 1 METYNAMIGYZLQAREFLERRERPARHGYASLCPHHSPOTYCRRRRPPLQAPONLNSGRS 60 MEPHASYIGVILQAREFLERERERENGYASICPH SPG + RRHK P QARGA + 16AS Sbjc: 56 MEPHASYIGVILQAREFLERERERENGYASICPHRSPGPIHRRUGREPGAPGAGGSGAS 235 Quary: 61 VHNELEKRRRAÇLKROLEGLACOMPLOVOCTRYTYLELL-KARVHICKLEDGEGGARRIX 119 VNNELEXARRAGLERCLE+L+OCMPLG OC RYTYLIGL RARHITOSTLE+GEG-RAN-LK
551ct: 236 VNNELEXARRAGLERCLERLKOCMPLGGOCAAYTTLELLRRARHHIOXLEOGGORAAGLK 416 Quecy: 120 EKLES 124 C+TB4 Spict: 416 ERLET #30 GB] [CD2407] CO2407 NUMGS0D12279, Numer Gene Signature, 3'-directed cDNA asquence. Length - 340 Score = 91.5 tite (239), Expect = 6e-70 Identities - 61/60 (808), Positives - 56/63 (678) Query: 106 KQQSLQQQLEQLQGLFGARERCALRADELDSBGLSFERSOSDQLDLEVDVENSVFGTETE 184 ROOSLOF CLFOL ON EMERIPADELDESGLESERSDEDOGHLEVOVEFLVIG E E Bbjot: 45 KOOSLOROPHOLRGLADAAERERLRADSLOASGLSSERSDSDOCCLEVDVESLVFOGEAE \$24

Figure 17 A

Query: 185 LLQ 187 LL+ Styct: 225 LLR 233 BASE COUNT 130 B 234 c 258 g 106 t 5 others DRIGIN 1 cagoogotty ctooggoogy canoctages cycagteege caggetyteg coparatega 61 accortoger agraecator agateraget graggonger ganttoring agreentes 121 gagagaggec gagestggtt atgesteect stseedest escapteeas secreteea 181 caggaggaag aagegaccee cecaggetee tggcgcgcap gacageggge ggtdagtgca 2:1 caatgaacty gagaagegea ggagggeeea yttpaagegg tgeetggage ggetgaagea 301 gragatgece etgggeggeg actgtgeeeg gtacacearg etgagretie tiergeegtge 361 caggargcac atockgolgc tggaggarca ggagcagcqq precederage teakggagag 421 gotgegeses asgesgesgs gestgesges gesstagstg cagetoeggg ggetggesga 481 ngeggeegga egggsgegga eagtetggse tecteaggee teteetega 541 gogotcagae teagaccaag appagetaga ggtggatgtg gagageetagg tgtttggggg 601 tgaggeogag etgetgeggg gettegtege eggeoaggag cacagetact eggacgtegg 661 eggegeetgg etatgatgtt ecteaccean ggegggeete tgeetetta etagttgeee 721 aageceaett the

Figure 17B



D

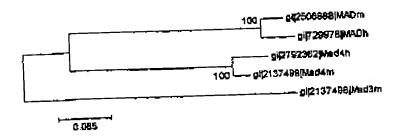
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Mzplasniqvliqaaeflerrerzaehgyaslophropgihrrkkrppgafgaqdsgrsvhnelekrrraqlk rclerlkqomplggdcaryttusllrrarmhiqkledqeqrarqlkerlrtkgoslorxwmqlrglagaaerer lradsldssglssersdsdoeelevdveslvfggeaellrgfvagoehsyshvggarl

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q1 7506148 RADs q1 779971 RADs q1 779975 Redf2 q1 779975 Redf2 q1 23371 Redf4 q1 23371 Redf4 q4 23371 Redf4 Hed3h Potetive	-ngylardi (antyny), fyrfytar niarzkoanizko (hrókka adpocacher ang terminian nigyka togocak i 1777) kylargi (antyny), fyrfyt i 1906 fyr na 2000 kalandak 1906 kalandak 1906 kalandak i 1906 kalandak i 1906 kaland
93 (350anns Japan 95 (783976 (1950a 93 (3793367 (1960a) 93 (35574 90 (1960a) 94 (35374 90 (1960a) 1963); Potat Sun	reyaes (kriocog); rotes e electroscologiscol
gi (2504846) Mike giri (25176) Mike giri (25176) Mike giri (21376) Mike giri (21376) Mike Mike (21376) Mike Mike (21376) Mike Mike (21376) Mike Mike (21376) Mike Mike (21376) Mike (21376)	Vyusdirastyje 16—suriy 13 at vysakrajdo maddici Vsusdirastych 16—suriy 13 f 14 hai klajdokradici Strandny 16 deg vyrang 16 gradikloh 16 klassica Strandny 16 deg vyrang 17 deg 18 klassica Variy 18 klassica

Figure 17 C-D

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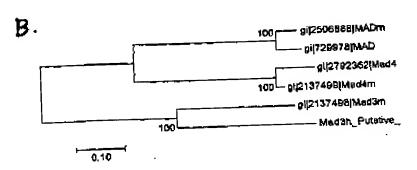


Figure 18-A-B

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% lexsemsub.pl
% lexsemaub.pat
% revised March 17, 2000
            LEXICON OF SUBSTANCES AND STRUCTURES
:-multifile(phrase/5).
:-multifile(wdef/3).
:-unknown( ,fail).
phrase('[',protein, ['[',gamma,']','-',aminobutyric, acid, a], 'GA
BAA', r}, % ?
phrase('[',smallmolecule, ['[',zeta,']',1, subunit], '[zeta]1 subu
nit', r). % ?
phrase(116, protein,[116,'-',kd,fyn,'-',associated,protein],'116-k
D Fyn-associated protein',r }.
phrase(l16, protein,[116,'-',kd,protein], 'l16-kd protein',r).
phrase(3,protein, [3,'-',kinase,'-',akt], '1-kinase-Akt',r).
phrase (ability, affirmation, [ability, to], [], r).
phrase (agc, protein, [agc, protein, kinases], 'AGC', r).
phrase(akt,protein, [akt, mutant], 'Akt mutant', r).
phrase(alternative, substance, [alternative, ntf], 'alternative NTF', r
phrase (antibody, protein, [antibody, to, phosphotyrosine], 'anti-phosp
hotyrosine',r).
phrase (antigen, complex, [antigen, receptor], 'antigen receptor', r).
phrase(ap, protein, [ap, '-', 1], 'AP-1', r).
phrase (aspargine, site, [aspargine, '-', 141], 'aspargine-141', r).
phrase(b, cell, (b,cell), 'B cell', r).
phrase(b, cell, (b,cells), 'B cell', r).
phrase(b, species,[b,lymphoblastoid,cells], 'B lymphoblastoid cell
phrase (b, cell, (b, lymphoblastoid, cells), 'B lymphoblastoid cells', r
phrase(b7, protein, [b7,'-','l'], 'B7-l',r).
phrase(bcl,protein,[bcl,'-',2],'Bcl-2',r).
phrase(c, protein, [c,'-',jun] , 'c-Jun',r).
phrase(camk, protein, [camk, iv], 'CaMK IV',r).
phrase(casp, protein, [casp, '-', 3], 'caspase-3', r).
phrase(caspase.protein,[caspase.'-'.3,family.protease], 'caspase-3
 family protease',r).
phrase (caspase, protein, [caspase, '-', 3, precursor], 'caspase-3 precur
phrase (caspase, protein, [caspase, '-', 3], 'caspase-3', r).
phrase {caspase, protein, [caspase, -, 3], 'caspase-3', r).
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Appendix A

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phrase (caspase, protein, (caspase, '-', 6], 'Caspase-6', r).
phrase (caspase, protein, [caspase, '-', 7], 'caspase-7', r).
phrase(catalytic, domain, [catalytic, domain], 'catalytic domain',
r).
phrase(cleavage, site, (cleavage, site), 'cleavage site',r).
phrase(cleavage, substance, [cleavage, products], 'cleavage products',
r).
phrase(cooh, substance, [cooh, '-', terminal, fragment], 'COOH-termina
l fragment',r).
phrase(crk,protein,[crk,proteins], 'crk proteins',r0.
phrase(crk1, complex,[crk1,'-',c3g,complex],'crk1-c3g complex',r).
phrase (dcp, protein, [dcp, -, 1], 'DCP-1', r).
phrase (did, negation, [did, not], not, r).
phrase (ebv.species, 'Epstein-Barr virus',r).
phrase (epstein, species, [epstein, '-', barr, virus], 'Epstein-Barr vi
rus',r).
phrase (familial, disease, [familial, alzheimer, '''', a, disease), 'famil
ial Alzheimer'''s disease',r).
phrace (gene, gene, [gene, encoding, interleukin, '~',2], 'gene encodin
g interleukin-2', r).
phrase(gst, protein, [gst,'-','fyn','-',sh2], 'GST-Fyn-SH2',r).
phrase(gst, protein, [gst,'-','fyn','-',sh3], 'GST-Fyn-SH3',r',
phrase(gtp, complex,[gtp,exchange.of,rapl], GTP exchange of Rapl',
r).
phrase (quanidine, protein, [guanidine, nucleotide, '-', releasing, fac
tor.c3g], 'guanidine nucleotide-releasing factor C3G1,r).
phrase (quanidine, smallmolecule, [quanidine, nucleotide], 'quanidine
 nucleotide',r).
phrase (quanosine, smallmolecule, [guanosine, triphosphate], 'guanosin
e triphosphate', r).
phrase (guanosine, smallmolecule, [guanosine, diphosphate], 'guanosine
diphosphate',r).
phrase(h4.cell,[h4.cell,line], 'H4 cell line',r).
phrase (h4, cell, [h4, human, neuroglioma, cells], 'H4, human, neuroglioma
,cells',r}.
phrase(ha, protein, [ha, '-', '[',delta,']',phpkb], 'HA-[Delta]PHPK
B',r).
phrase(hla, protein, [hla,'-',dr7], 'HLA-DR7',r).
phrase(i, protein, [i, '[',kappa, ']',b,'-','[',beta,']'),
                                                                'I[ka
ppa|B-[beta]',r).
phrase(i,protein, [i, '[',kappa, ']',b,'-','[',alpha,']'],
pa]8-[alpha]',r).
phrase(i,protein, [i, '[',kappa, '|',b], 'I(kappa]B',r).
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phrase(ice,protein,[ice,'/',ced,'-',3),'1CE/Ced-3',r),
phrase(il, gene, [il,'-',2.gene), 'gene encoding interleukin-2', r
phrase(il, protein, [il,'-',2], 'interleukin-2',r).
phrase(in, interm, [in, the, case, of],[], r).
phrase(in, state, [in, the, anergic, state], inactive, r).
phrase(inducible, cell, [inducible,h4,cell], 'inducible H4 cell',r
phrase {interleukin, protein, [interleukin, '-',2],r).
phrase (interleukin, protein, (interleukin, '-', 3], 'interleukin-3
phrase(interleukin,protein,[interleukin,'~',1,beta,converting,enzy
me], 'interleukin-1 beta converting enzyma',r).
phrase(jurkat, cell, [jurkat, cell], 'Jurkat cell', r).
phrase(jurkat, cell, (jurkat, cells), 'Jurkat cell', r).
phrase(kif3a,protein,[kif3a,'/',3,b],'KIF3A/3B',r).
phrase(ibl, cell, [lbl,'-',drf, cells], 'LBL-DR7 cella',r).
phrase(1bl,cell,[1bl,'-',dr7,cells],'LBL-DR7 cells',r).
phrase(let, protein, [let, '-', 23], 'Let-23', r).
phrase(may, probability, [may, be], possible, r).
phrase(myc, protein, [myc, '-', p70s6kd3e], 'Myc-p70s6kD3B',r).
phrase(myc, protein, {myc, '.', pdkl], 'Myc-PDK1',r}.
phrase (myc, protein, [myc, '-', p?bs6k], 'Myc-p?bs6k', r).
phrase(myc,protein,[myc,'-',p70s6ke389d3e], 'Myc-p70s6kE389D3E',r)
phrase(myr, protein, [myr, '-', akt], 'Myr-Akt', r).
phrase(n.protein. [n.'-'.methyl.'-'.d.'-'.aspartate, receptor], 'N
MDAR', r.
phrase(n.protein, {n,'-',methyl,'-',d,'-',aspartate], 'NMDA'},
phrase(native, cell, [native, h4, cell], 'native H4 cell', t).
phrase(nf, protein, [nf,'-','[',kappa,']',b], 'NF-[kappa]8',r),
phrase(nh2, site, [nh2,'-',terminal], 'NH2-terminal',r).
phrase(nh2, substance, [nh2, '-', terminal, fragment], 'NH2-terminal fr
agment', r).
phrase(nih, cell, [nih,'-',3,t3,fibroblasts], 'NIH-3T3 fibroblasts'
phrase(nih,cell,[nih,'-','3t3', fibroblasts],'NIH-3T3 fibroblasts'
phrase(normal, substance, [normal, ntf], 'normal NTF', r).
phrase(nuclear, protein, [nuclear, factor, kappa, b],'NF-[kappa]B'
phrase(pl50Glued,protein,[pl50Glued,-,arp1],'p150Glued-Arp1',r).
phrase(phosphate,phosphorylate2, [phosphate, incorporated, intn],
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phosphorylate,r).

phrase (phosphatidylinositol, smallmolecule, [phosphatidylinosito], 1 ,',',4,',',5,'-',triphosphate), 'phosphatidylinositol 1,4,5-tripho aphate',r). phrase (phosphoinositide, protein, [phosphoinositide, '-', dependent, protein, kinase), 'PDK1',r). phrase(phospholipase, protein, [phospholipase,c,'-',1],'phospholip ase C-1', r): phrase(poly,protein, [poly, '{',adp, '-',ribose,')',polymerase], 'poly (ADP-ribose) polymerase',r}. phrase(polyvinylidene, structure; [polyvinylidene, difluoride, memb ranes), 'polyvinylidene difluoride membranes', r). phrase(presentlin, protein, [presentlin, 1], 'presentlin 1',r). phrase(presentlin, protein, [presentlin, 2], 'presentlin, 2', r). phrase(productively, state, [productively, stimulated], active, r). phrase(protein, protein, [protein, tyrosine, kinase], 'protein tyrosi πe kinase', r). phrase(protein, protein, [protein, kinase, c], 'protein kinase C', r). phrase(ps2, substance, [ps2, '-', ctf], 'presentlin 2 COOH-terminal fra phrase(ps2, substance, [ps2,cleavage, fragment], 'presenilin 2 cleava qe fraqment', r). phrase(pvdf, structure, [pvdf, membranes], 'polyvinylidene difluori de membranes',r). phrase(raf, protein, [raf,'-',1], 'Raf-1', r). phrase(raf,protein, [raf,'-',1], 'Raf-1',r). phrase(rap1.complex,[rap1,'-',gtp), 'Rap1-GTP',r). phrase(requirement, need2, [requirement, for], need,r). phrase(ser, smallmolecule, [ser, 19], 'Ser 19',r). phrase(ser, smallmolecule, [ser, 23], 'Ser 23',r). phrase(serine, substance, [serine, residues], 'serine residues', r phrase(src, domain, [src, homology, 2], 'Src homology 2',r). phrase(src, domain, (src, homology, 3], 'Src homology 3',r). phrase(srebp,protein,[srebp,'-',1], 'sterol-regulatory element bin ding protein 1',r). phrase(srebp,protein,[srebp,'-',2], 'sterol-regulatory element bin ding protein 2',r). phrase (sterol, protein, (sterol, '-', regulatory, element, binding, prote in, 1], 'sterol-regulatory element binding protein 1', r). phrase (sterol, protein, [sterol, '-', regulatory, element, binding, prote in,2], 'sterol-regulatory element binding protein 2',r).

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phrase(t, cell, [t,'-',dr7], 't-DR7',r).
phrase(t, cell, [t,'-',drt,'/',b7,'-',1],'t-DR7/B7-1',r).
phrase(t, cell, [t,cell], 'T cell',r).
phrase(t, cell, [t,cells], 'T cell',r).
phrase(t, complex, (t,'~',cell,receptor),'T-cell receptor',r).
phrase(t,cell,[t,'-',dr7, cells],'t-DR7 cells',r).
phrase(t,cell,[t,'-',dr7,'/',b7,'-',1], 't-DR7/B7-1',r).
phrase(t,complex,[t,'.',cell,antigen,receptor),'T-cell antigen red
eptor', r}.
phrase (threonine, aminoacid, [threonine, 229], 'threonine 229', r)
phrase(transcription, protein, [transcription, factor], 'transcript
ion factor', r}.
phrase(trypan, smallmolecule, 'trypan blue', r).
phrase(wt, protein, [wt, akt], 'WT Akt',r).
phrase(zap, protein, [zap, '-', 70], 'ZAP-70', r).
phrase(zdevd, smallmolecule, [zdevd, '-', fmk], 'zDEVD-fmk',r).
phrase(il, protein,[il,'-',3],' interleukin-3',r).
wdef(ab, complex, antibody).
wdef(actin,protein,actin).
wdef(activated, state, active).
wdef(active, state, active).
wdef(ad, disease, 'Alzheimer''''s disease').
wdef(agc,protein, 'AGC').
wdef(akt, protein, 'AKT').
wdef(amergic, state, inactive).
wdef(amergic, etate, inactive).
wdef(amergy, state, inactive).
wdef (antibody, complex, antibody).
wdef(antigen, substance, antigen).
wdef(aop, protein, 'Aop').
wdef(apoptosis,process,apoptosis).
wdef(bad, protein, 'BAD').
wdef(c3g, protein, 'C3G').
wdef('ca2+', smallmolecule,'Ca2+').
wdef(cas, protein, 'Cas').
wdef(caspase, protein, caspase).
wdef(caspase, protein, caspase).
wdef(cbl, protein, 'Cb1').
wdef(ccrsrh,protein,'CCRSrh').
wdef(cd28, protein, 'CD28').
wdef(cells, structure, cell).
wdef(cholesterol, smallmolecule, cholesterol).
```



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wdef(cpp32,protein,'CPP32').
 wdef(crkl, protein, 'CrkL').
 wdef(ctf, substance, 'COOH-terminal fragment').
 wdef(cytokine, smallmolecule, cytokine).
 wdef(cytosol, structure, cytosol).
 wdef(djnk, protein, 'DJNK').
 wdef{djun, protein, 'DJun'}.
 wdef (dynamitin, protein, dynamitin).
 wdef(erk, protein, 'ERK').
 wdef(eto,smallmolecule,'ETO').
 wdef (etoposide, smallmolecule, etoposide).
 wdef(fad, disease, 'familial Alzheimer'''s disease').
 wdef(fyn, protein, 'Fyn').
 wdef(qdp, smallmolecule, 'GDP').
 wdef (gelaolin, protein, gelsolin).
 wdef(ap120, protein, 'gp120').
 wdef{grb2, protein, 'Grb2').
 wdef(qst, protein, 'glutathione S-transferase').
 wdef (gtp, smallmolecule, 'GTP').
 wdef (hap70, protein, 'HSP70').
 wdef(human, species, human).
 wdef(ikk, protein, 'IKK').
 wdef(inactivated, state, inactive).
 wdef (inactive, state, inactive).
 wdef(jnk, protein, 'JNK').
 wdef(jnk, protein, 'JNK').
 wdef(jnk2, protein, 'JNK2').
 wdef(kap3, protein, kap3).
 wdef(kdakt, protein, 'KDAkt').
 wdef(kinase, protein, kinase).
 wdef (kinectin, protein, kinectin).
 wdef(klc,protein,klc).
, wdef(lamin,protein,lamin).
 wdef (myosins, protein, myosins).
 wdef(nmdar,protein, 'NMDAR').
 wdef(nmdar2b, protein, 'NMDAR2B').
 wdef(ntf, substance, 'NH2-terminal fragment').
 wdef(p70s6k, protein, p70s6k).
 wdef(p78s6k, protein, p78s6k).
 wdef(parp,protein, 'poly(ADP-ribose)polymerase').
 wdef(pdk1, protein, 'PDK1').
 wdef (peptides, protein, peptide).
 wdef(pkb, protein, 'PKB').
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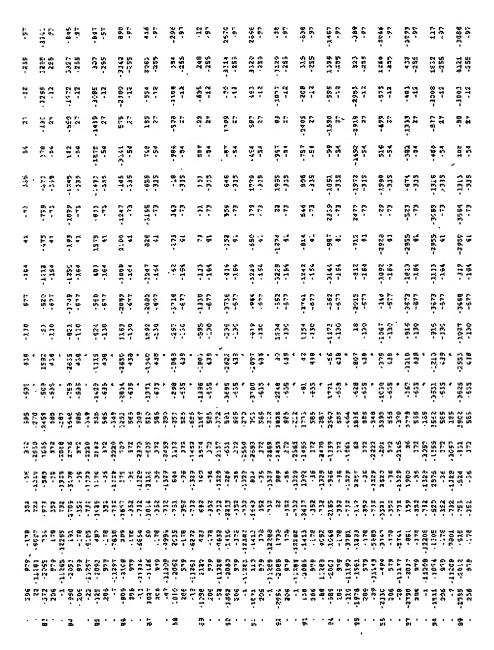
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-2751	323	-4142	333	373	-3560	1159	373	-2859	106	372	-1799	-1199	372	7695	-2120	372	-37b6	767	372	-370E	-3130	373	-3706	-853	3.12	-3206	-4130	373	-370£	-514	372	1962-	- 344	372	-3629	-146	372	-3636	-372	373	-9916	-750	372	-2264
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wdef(pkc,protein, 'protein kinase C').
wdef(position, site, site).
wdef(positions, site, site).
wdef (protease, protein, protease).
wdef (psl, protein, 'presenilin 1').
wdef (ps2, protein, 'presenilin 2').
wdef(rapl, protein, 'Rapl').
wdef(ras, protein, 'Ras').
wdef(receptors, substance, receptor).
wdef(rela, protein, 'RelA').
wdef (residues, substance, residue).
wdef(responsive, state, active).
wdef($6, protein, 'S6').
wdef(selectively, constraint, selective).
wdef(ser112, site, 'Ser112').
wdef(ser136, site, 'Ser136').
wdef(ser32, smallmolecule, 'Ser32').
phrase(ps1, protein
wdef(ser36, smallmolecule, 'Ser36').
phrase(ps1, protein, [ps1,'-',ctf], 'ps1-ctf',r).
wdef(sh2,domain, 'SH2').
wdef(sh3,domain,'SH3').
wdef(shc, protein, 'Shc').
wdef(signalsome, complex, signalsome).
wdef (sites, site, site).
wdef(sos, protein, 'Sos').
wdef (staurosporine, smallmolecule, staurosporine).
wdef(sts, smallmolecule, 'STS').
wdef(tcr, complex, 'T-cell receptor').
wdef (tetracycline, smallmolecule, tetracycline).
wdef(thr229, aminoacid, 'Thr229').
wdef (thr308, aminoacid, 'Thr308').
wdef(thr389, aminoacid, 'Thr389').
wdef (threonine, aminoacid, threonine).
wdef(tyrosine, aminoacid, tyrosine).
wdef {unresponsive, state, inactive}.
wdef (unstimulated, state, inactive).
wdef(zvad, smallmolecule, 'zVAD').
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% lexsyn.pat
% revised March 17, 2000
                 SYNTACTIC LEXICON FOR ACTIONS
% Contains syntactic entries for action type words and phrases
% symp (+Word1.+Wordlist,+Sym)
& symp: Wordl is first word of phrase, Wordlist is list of words i
n phrase
& synp: Syn is syntactic categorey
& synw(+Word,+Syn) is same as synp except there is no wordlist
symp (account, [account, for], v).
symp (account, [account, for], vp).
symp (accounted, [accounted, for], ved).
symp(accounted, [accounted, for], ven).
symp(accounting, {accounting, for), ving).
eynp (accounting, (accounting, for), n).
eynp (accounts, [accounts, for), vp).
aynp(add, [add, up], vp).
aynp (add, [add, up], v).
symp (added, [added, up],, ved).
symp(added, [added, up], ven).
eynp (adding, [adding, up], n).
symp(adding, [adding, up], ving).
symp(adds, [adds, up].vp).
symp(am, [am,a,means,of, producing],vp).
symp(am, [am, due, to], vp).
symp(are, {are,a,means.of, producing).vp).
symplare, (are, due, to), vp).
symp(as, [as, a, result, of], prep).
symp(attributable,[attributable,to],vp). % ?
symp(attributed, [attributed, to], ven).
symp (based, [based, on], ven).
synp (based, [based, upon], ven).
symp(be, [be,a,means,of, producing),v).
symp(be, [be,due,to],v).
synp (because, [because, of], prep).
symp(been, [been, a, means, of, producing), ven).
synp (been, [been, due, to], ven).
synp(being, [being, a, means, of, producing], n).
symp(being, [being, a, means, of, producing], ving).
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Appendix B

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symp(being, [being, due, to], n).
symp(being, [being, due, to], ving).
symp(caused, [caused,by],ved).
symp(caused; [caused,by],ven).
symp(convey, [convey, a, signal], v).
symp(convey, (convey, a, signal), vp);
symp (conveyed, (conveyed, a, signal), ved).
symp(conveyed, [conveyed, a, signal], ven).
symp(conveying, (conveying, a, signal), ving).
symp(conveying, (conveying, a, signal), n).
symp(conveys, [conveys,a, signal], vp).
symp(dissociate, [dissociate, from], vp).
synp(dissociate, [dissociate, from], v),
symp(dissociated, [dissociated, from], ved).
symp (dissociated, [dissociated, from], ven].
synp (dissociates, [dissociates, from], vp).
symp (dissociating, [dissociating, from], n).
symp(dissociating, [dissociating, from], ving).
symp (dissociation, [dissociation, from], n).
symp(down, [down, '-', regulate], v).
synp (down, [down, '-', regulate], vp).
                                      % A down-regulates B
symp{down, {down, '-', regulated}, ved).
symp(down, [down, '-', regulated], ven).
symp (down, [down, '-', regulates], vp).
symp(down, [down, '-', regulating], n).
symp(down, [down, '-', regulating], ving).
symp(down, [down, '-', regulation], n).
symp(due, [due, to, the, fact, that], adj).
synp (due, [due, to], adj). % ?
symp(form, [form, complex], v),
symp(form, [form, complex], vp).
symp (formation, [formation, of, complex], n).
symp{formed, [formed, complex], ved).
symp(formed, [formed, complex), ven).
symp{forming, [forming, complex],n).
symp(forming, [forming, complex], ving).
symp(forms, {forms, complex}, vp).
symp(had, [had,an,active,role,in],ved).
symp(had, [had,an,active,role,in],ven).
symp(has, [has,an,active,role,in],vp).
symp(have, [have, an, active, role, in], v).
symp(have, [have,an,active,role,in],vo).
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symp(having, [having, an, active, role, in], n).
symp(having, [having, an, active, role, in], ving).
symp(is, [is,a,means,of, producing],vp).
eynp(is, [is,due,to],vp).
symp (functions, [functions, as, a, negative, regulator, of], vp).
symp (function, [function, as, a, negative.regulator, of].vp).
symp(lead, [lead,to],v).
symp(leads, [leads,to],vp).
symp(leading, [leading,to],n).
gymp(leading, [leading,to], ving ).
eynp(leads, [leads,to],vp).
symp(led, [led, to], ved).
aynp (led, [led, to], ven).
eymp(may, [may, be, responsible, for], vp).
                                              %A mediates a signal to
synp(mediate,[mediate, a, signal], v).
symp(mediate, [mediate, a, signal], vp).
synp(mediated, [mediated, a, signal], ved).
synp(mediated, [mediated, a, signal], ven).
symp (mediates, [mediates, a, signal], vp).
symp (mediating, [mediating, a, signal], n).
symp(mediating,[mediating, a, signal], ving).
symp(mediation, [mediation, of, a, signal], n).
symp(n, (n, '-', acetylate), v).
symp(n, [n, '-', acetylate], vp).
symp(n, [n, '.', acetylated], ved).
symp(n, [n, '-', acetylated], ven).
symp(n, (n, '-', acetylates).vp).
symp(n, [n, '-', acetylating), n).
symp(n,[n,'-',acetylating],ving).
symp(n,[n,'-',acetylation],n).
symp(n, [n, '-', acylate], v).
symp(n, [n, '-', acylate], vp).
symp (n, [n, '-', acylated), ved).
symp (n, [n, '~', acylated], ven).
symp(n, [n, '-', acylates], vp).
symp(n, [n, '-', acylating], n).
symp(n, [n, '-', acylating], ving).
symp(n, \{n, '-', acylation\}, n).
synp(n, (n, '-', glycosylate), v).
symp(n, [n, '-', glycosylate], vp).
symp(n, [n, '-', glycosylated), ved).
symp(n, {n, '-', glycosylated), ven).
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symp(n, [n, '-', glycosylates], vp).
symp {n, [n, '-', glycosylating], n}.
symp(n, [n, '-', glycosylating), ving).
symp \{n, \{n, '-', g\}\}\ symp \{n, \{n, '-', g\}\}\.
symp (n, [n, '-', terminal, proteolysis), n).
symp(o, [o, '-', qlycosylate], v).
symp(o, (o, '-',glycosylate),vp).
symp(o, (o, '-', glycosylated), ved).
symp (o, [o, '-', glycosylated], ven).
symp(o, [o, '-', glycosylates], vp).
symp(o, [o, '-'.glycosylating],n).
symp(o,[o,'-',glycosylating],ving).
symp (o, [o, '-', glycosylation], n).
symp(only, (only, after), prep).
symp(prolyl, (prolyl,'-',4,'-',hydroxylate),v ).
symp(prolyl, [prolyl, '-',4,'-',hydroxylate],vp).
symp(prolyl, (prolyl,'-',4,'-',hydroxylated), ved ).
symp(prolyl, [prolyl, '-',4,'-', hydroxylated], ven ).
synp(prolyl, [prolyl, '-',4,'-',hydroxylates],vp).
symp{prolyl, (prolyl, '-',4,'-',hydroxylating],n ).
symp(prolyl, [prolyl,'-',4,'-',hydroxylating],ving ).
symp(prolyl, [prolyl,'-',4,'-',hydroxylation],n).
symp(result, [result, from], v).
symp(result, [result, from], vp).
symp(result, [result, in], v).
symp(result, [result, in], vp).
symp(resulted, [resulted,from], ved).
symp (resulted, [resulted, from], ven).
symp(resulted, [resulted,in],ved).
symp(resulted, [resulted, in], ven).
symp(resulting, [resulting, from], n).
symp(resulting, [resulting, from] , ving).
symp(resulting, [resulting, in], n).
symp (resulting, [resulting, in], ving).
symp(results, [results,from], vp).
symp(results, [results,in], vp).
symp(set, [set, free],v).
symp(set, [set, free].v).
symp(set, [set, free], ved).
symp(set, [set, free], ved).
symp(set, [set, free], ven).
synp(sét, [set, free], ven).
symp(set, [set, free], vp).
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eynp(set, [set, free], vp).
symp(sets, [sets, free], vp).
symp(sets, [sets, free], vp).
symp(setting, [setting, free], n).
symp(setting, (setting, free),n).
symp(setting, [setting, free], ving).
symp(setting, [setting, free), ving).
symp(suppress, (suppress, activity, of), v).
symp(suppress, [suppress, activity, of], yp).
symp(suppressed, [suppressed, activity, of), ved).
symp(suppressed, [suppressed, activity, of], ven).
symp(suppresses, [suppresses, activity, of], vp).
symp(suppressing, [suppressing, activity, of], n).
symp(suppressing, [suppressing, activity, of], ving).
symp(suppression, [suppression, of, activity, of], n).
symp(switch, [switch, on, the, activity, of], vp).
symp(switched, (switched, on, the, activity, of), ved).
symp(switched, (switched, on, the, activity, of), ved).
eynp(switched,[switched, on, the, activity, of], ved).
symp(switched,[switched, on, the, activity, of], ved).
symp(switched, [switched, on, the, activity, of), ved).
symp(switches, (switches, on, the, activity, of), vp).
symp(up, [up, '-', regulate], v). % A up-regulates B B --> A
eymp(up, |up, '-', regulate|, vp). % A up-regulates B B --> A
symp (up, (up, '-', regulated), ved).
symp(up, (up, '-', regulated), ven). % A up-regulates B B --> A
symp (up, [up, '-', regulates], vp).
symp (up, (up, '-', regulating), n). & A up-regulates B B --> A
symp(up, {up, '-', regulating), ving). % A up-regulates B B --> A
symp(up, (up, '-', regulation), n).
synp(was, [was,a,means,of, producing], ved).
symp(was, [was,due,to], ved).
eymp(were, [were,a,means,of, producing],ved). % ?
symp(were, [were, due, to], ved).
synw(acetylate, v).
synw(acetylate, vp).
synw(acetylated, ved).
synw(acetylated, ven).
synw(acetylates, vp).
synw(acetylating, n).
synw(acetylating, ving).
synw(acetylation,n).
synw(activate, v).
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synw(activate, vp).
synw(activated, ved).
symw(activated, ven).
synw(activates, vp).
synw (activating, n).
synw(activating, vinq),
synw (activation, n).
synw(add,v).
synw(add, vp).
synw(added, ved).
synw(added, ven).
synw(adding, n).
synw(adding, ving).
synw(addition,n).
synw (adds, vp).
synw(after,prep).
synw(aggregate , v).
synw(aggregate ,vp).
synw(aggregated , ved).
synw(aggregated , ven).
synw(aggregates, vp).
synw(aggregating ,n).
synw(aggregating ,ving).
synw(aggregation ,n).
synw(arrest,n).
aymw(arrest, v).
synw(arrest, vp).
aynw(arrested, ved).
aynw(arrested, ven).
synw(arresting, n).
synw(arresting, ving).
synw(arrescs, vp).
svnw(associate.v).
synw(associate.vp).
synw (associated, ved).
synw(associated, ven).
Bynw(associates, vp).
synw (associating, n).
synw(associating, ving).
synw(association,n).
synw(attach , v).
synw(attach, vp).
synw(attached , ved).
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synw(attached , ven) .
synw(attaches, vp).
synw(attaching ,n).
synw(attacking , ving).
synw(attachment,n).
eynw(bind,v).
synw(bind, vp).
synw(binding,h).
synw(binding, ving).
synw(binds, vp).
synw(block, v).
synw(block.vp).
synw(blockage,n).
synw(blocked, ved).
synw(blocked, ven).
synw(blocking,n).
synw (blocking, ving).
synw{blocks, vp}.
synw(bound, ved).
synw(bound, ven).
synw(break, v).
synw(break, vp).
synw(breakage, n).
synw(breaking,n).
synw(breaking, ving).
synw(breaks, vp).
synw(broke, ved).
synw(broken, ven).
synw(catalyzation, n).
synw(catalyze, v).
aynw{catalyze,vp}.
synw(catalyzed, ved).
synw(catalyzed, ven).
synw(catalyzes, vp).
synw(catalyzing, n).
synw(catalyzing, ving).
svnw(causation.n).
synw(cause,n).
eynw(cause,v).
synw(cause, ven).
synw(cause, vp).
synw(caused, ved).
synw(causes, vp).
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eynw(causing, n). .
synw(causing, ving).
synw(cleavage, n).
synw(cleave, v).
synw(cleave, vp).
synw(cleaved, ved).
synw(cleaved, ven).
symw(cleaves.vp).
symw(cleaving, n).
synw(cleaving, ving).
eynw(coimmunoprecipitate ,v).
aynw(coimmunoprecipitate, vp).
synw(coimmunoprecipitated , ved).
synw(coimmunoprecipitated , ven).
synw(coimmunoprecipitates, vp).
synw(coimmunoprecipitating ,n).
synw(coimmunoprecipitating , ving).
synw(coimmunoprecipitation ,n),
synw(combination ,n).
synw(combine , v).
synw(combine .vp).
synw(combined , ved).
synw(combined , ven).
synw(combines, vp).
synw(combining ,n).
synw(combining , ving).
synw(conjugate ,v).
synw(conjugate , vp).
synw(conjugated , ve).
synw(conjugated , ved).
synw(conjugates, vp).
synw(conjugating ,n).
synw(conjugating , ving).
synw(conjugation ,n).
synw(connect , vp).
synw(connect, v).
synw(connected , ve) . - -
synw(connected , ved).
synw(connecting ,n).
synw(connecting , ving).
synw(connection ,n).
synw(connects, vp).
synw(constrain, v).
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gynw(constrain, vp).
eynw(constrained, ved).
synw (constrained, ven).
eynw(constraining,n).
synw(constraining, ving).
eynw(constrains, vp).
synw(constraint, n).
synw(coprecipitate, v).
synw(coprecipitate, vp).
synw (coprecipitated, ved) .
synw(coprecipitated, ven).
synw(coprecipitates, vp).
synw(coprecipitating,n).
synw(coprecipitating, ving).
synw{coprecipitation ,n).
synw(copurification ,n).
synw{copurified , ved).
synw(copurified , ven).
synw (copurifies, vp).
synw(copurify , vp) .
synw(copurify, v).
synw(copurifying ,n).
synw(copurifying , ving).
synw(couple ,Vp).
synw(couple, v).
synw(coupled, ved).
synw(coupled, ven).
synw(couples, vp).
synw(coupling, n).
synw(coupling.ving).
synw(cut,n).
synw(cut,v).
synw(cut, ved).
synw(cut, ven).
synw(cut, vp).
synw(cuts, vp).
synw(cutting,n).
synw(cutting, ving).
synw(deactivate, v).
synw(deactivate, vp).
synw(deactivated, ved).
synw (deactivated, ven) .
synw(deactivates.vp).
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synw(deactivating,n).
synw(deactivating, ving).
Bynw{deactivation,n).
synw (death, n).
synw (demethylate, v).
synw (demethy late, vp).
synw (demethylated, ved).
synw (demethylated, ven).
synw (demethy lates, vp).
synw(demethylating,n).
synw (demethylating, ving).
synw(demethylation, n).
synw(dephosphorylate, v),
synw{dephosphorylate, vp}.
synw(dephosphorylated, ved).
synw(dephosphorylated, ven).
synw(dephosphorylates, vp).
synw (dephosphorylating, n).
symw(dephosphorylating, ving).
synw(dephosphorylation, n).
synw(die,v).
synw (die, vp).
synw (died. ved).
synw(died, ven).
synw(dies, vp).
synw (disassemble, v).
synw(disassemble, vp).
synw{disassembled, ved).
synw (disassembled, ven).
synw(disassembles, vp).
synw(disassembling, n).
synw(disassembling, ving).
synw(disassembly, n).
synw(discharge, n).
synw(discharge, v).
synw(discharge, vp).
synw(discharged, ved):
synw(discharged, ven).
synw(discharges, vp).
eynw (discharging, n).
synw (discharging, ving).
synw(disengage, v).
synw(disengage, vp).
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synw{disengaged, ved}.
synw{disengaged, ven}.
synw(disengagement,n).
synw(disengages, vp).
synw (disengaging, n).
synw (disengaging, ving).
synw(divide, v).
synw (divide, vp).
synw (divided, ved).
synw{divided, ven}.
synw (divides, vp).
synw (dividing, n).
synw(dividing, ving).
synw(division, n).
synw(dying,n).
synw(dying, ving).
synw(enhance, v).
synw(enhance, vp).
synw (enhanced, ved).
synw(enhanced, ven).
aynw(enhancement, n).
synw(enhances, vp).
synw (enhancing, n).
synw(enhancing, ving).
synw(express,V).
aynw (express, vp).
synw(expressed, ved).
synw(expressed, ved).
synw (expressed, ven).
synw(expresses, vp).
synw(expressing,n).
synw(expressing,n).
synw(expressing, ving).
synw(expression, n).
synw(generate, v).
aynw(generate, vp).
synw(generated, ved).
synw (generated, ven).
aynw (generates, vp).
synw(generating,n).
synw(generating, ving).
synw (generation, n).
synw (hew, v).
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synw (hew, vp).
synw (hewed, ved)
synw (hewed, ven).
synw(hewing,n).
synw(hewing, ving).
aynw (hews, vp).
synw(hinder, v).
synw(hinder, vp).
synw(hindered, ved).
synw(hindered, ven).
synw(hindering,n).
synw(hindering, ving)...
synw(hinders, vp).
synw(hindrance, n).
synw(inactivate,v).
synw(inactivate, vp).
synw(inactivated, ved).
synw(inactivated, ven).
synw(inactivates, vp).
synw(inactivating,n).
synw(inactivating, ving).
synw(inactivation, n).
synw(incite, v).
synw (incite, vp).
aynw(incited, ved).
synw(incited, ven).
synw(incitement,n).
synw(incites, vp).
synw(inciting, n).
synw(inciting, ving).
synw (induce, v).
synw(induce, vp).
synw(induced, ved).
synw(induced, ven).
synw(induces, vp).
aynw(inducing, n).
synw(inducing, ving).
synw(induction, n).
synw (influence, n).
synw(influence, v).
synw(influence, vp).
synw{influenced, ved}.
aynw{influenced, ven}.
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synw(influences,vp)..
synw(influencing,n).
synw(influencing, ving). % ?
synw(inhibic, v).
synw(inhibit.vp).
gynw(inhibited, ved).
avnw(inhibited, ven).
aynw(inhibiting,n).
synw (inhibiting, ving).
gynw (inhibition, n).
gynw(inhibits, vp).
synw (initiate, v).
synw(initiate, vp).
synw(initiated, ved).
synw(initiated, ven).
synw(initiates, vp).
synw(initiating,n).
synw(initiating, ving).
aynw(initiation, vp).
synw(instigate, v).
synw (instigate, vp) .
synw(instigated, ved).
synw(instigated, ven).
synw(instigates, vp).
synw(instigating,n).
eynw (instigating, ving).
synw(instigation,n).
synw(interact, v).
synw(interact, vp).
synw(interacted, vec).
synw(interacted, ven).
synw (interacting, n).
synw(interacting, ving).
synw(interaction,n).
synw(interactions,n).
synw (interacts, vp).
eynw(join , vp).
symw(join,v).
synw(joined, ved).
aymw(joined,ven).
. (a, paining, n).
eynw(joining, ving).
evnw(joine,vp).
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synw(juncture, n).
synw(liberate,v).
synw(liberate, vp).
synw(liberated, ved).
synw(liberated, ven).
synw(liberates, vp).
 synw(liberating,n).
 synw(liberating, ving).
synw(liberation, n).
synw(limit, v).
synw(limit, vp).
synw(limitation, n).
synw(limited, ved).
synw(limited, ven).
synw(limiting, n).
synw(limiting, ving).
synw(limits, vp).
synw(link,n).
aynw(link,v).
synw(link,vp).
synw(linked, ved).
synw(linked, ven).
synw(linking, n).
synw(linking, ving).
synw(links, vp).
synw (mediate, v).
synw (mediate, vp).
synw (mediated, ved).
synw (mediated, ven).
synw (mediates, vp).
synw (mediating, n).
synw (mediating, ving).
synw (mediation, n).
synw (methylate, vp).
synw(methylate, v ).
synw (methylated, ved ).
synw(methylated, ven ).
synw (methylates, vp).
synw(methylating, n ).
synw(methylating, ving).
synw (methylation, n).
avnw(modification,n).
synw(modified, ved).
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synw (modified, ven).
synw (modifies, Vp).
synw (modify, v).
synw (modify, vp).
synw (modifying, n).
synw(modifying, ving).
synw (mutate, V).
synw(mutate, Vp).
synw (mutated, ved).
synw (mutated, ven).
synw (mutates, vp) .
synw (mutating, n):
synw(mutating, ving).
synw (mutation, n).
synw(overexpress,v).
synw (overexpress, vp).
synw (overexpressed, ved).
synw (overexpressed, ven) .
synw (overexpresses, vp) .
synw (overexpressing, n).
eynw (overexpressing, ving).
eynw(overexpression,n).
eynw(pair,v).
synw(pair, vp).
synw(paired, ved).
synw(paired, ven).
synw(pairing, n).
synw(pairing, Ving).
synw(pairs, vp).
synw(phosphorylate,n).
synw(phosphorylate,vp).
synw(phosphorylated, ved).
synw(phosphorylated, ven).
synw(phosphorylates,vp).
synw(phosphorylating,n).
synw(phosphorylating, ving).
synw(phosphorylation, n).
synw(promote, v).
synw(promote, vp).
aynw(promoted, ved).
aynw(promoted, ven).
synw (promotes, vp).
synw(promoting, n).
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synw(promoting, ving).
 synw(promotion,n).
 synw (prompt, n).
 synw(prompt, v).
 synw (prompt, vp).
 synw(prompted, ved).
 synw (prompted, ven).
 synw (prompting, n).
 synw (prompting, ving). .
 synw(prompts, vp).
 synw(react, v).
 synw(react, vp).
 synw(reacted, ved).
 synw(reacted, ven).
 Bynw (reacting, n).
 synw{reacting, ving}.
 synw (reaction, n).
 gynw (reacts, vp).
 synw (requlate, v).
 synw(regulate, vp).
 synw(requlated, ved).
 synw (regulated, ven).
 synw(regulates, vp).
 synw (regulating, n).
 symw(regulating, ving).
 synw(regulation,n).
 synw(release,n).
 synw(releage, v).
 synw(release, vp).
 synw(released, ved).
 synw (released, ven).
 synw(releases, vp).
 synw(releasing, n).
 gynw (releasing, ving).
 synw(removal,n).
 synw(remove, v).
 synw (remove, vp).
 synw(removed, ved).
 synw (removed, ven).
 synw (removes, vp).
. synw(removing,n).
 synw (removing, ving).
 synw(replace, v).
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synw (replace, Vp).
synw(replaced, ved).
synw(replaced, ven).
Bynw (replacement, n).
eynw(replaces, vp).
synw(replacing,n).
synw(replacing, ving).
synw(repress, Vp).
synw(repress, v).
synw (repressed, ved) .
synw (repressed, ven) .
synw (represses, vp).
synw(repressing, n).
synw(repressing, ving).
synw (repression, n).
synw(require, v).
synw (require, vp).
synw (required, ved).
synw(required, ven).
synw (requirement, n).
eynw (requires, vp).
aynw (requiring, n).
synw(requiring, ving).
synw(restrain, vp).
synw(restrain,v).
synw(restrained, ved).
synw(restrained, ven).
synw(restraining,n).
eynw(restraining, ving).
synw(restrains, vp).
synw(restraint, n).
synw(sensitization, n).
synw(sensitize, vp).
synw(sensitize, v).
synw(sensitized, ved).
synw(sensitized, ven).
synw(sensitizes, vp).
synw(sensitizing,n).
synw(sensitizing, ving).
synw(separate, v).
synw(separate, vp).
synw(separated, ved).
synw(separated, ven).
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aynw(aeparates, vp).
synw(separating,n).
synw(separating, ving).
synw(separation, n).
synw(sever, v).
synw(sever, vp).
synw(severance,n).
synw(severed, ved).
synw(severed, ven).
synw(severing.n).
synw(severing, ving).
synw(severs, Vp).
synw(signal,v).
synw(signal, vp).
synw(signaled, ved).
synw(signaled, ved).
synw(signaled, ven).
synw(signaling,n).
synw(signaling, ving).
synw(signale,vp).
synw(split,n).
synw(split,v).
synw(split, ved).
synw(split, ven).
synw(split, vp).
synw(splits.vp) . .
synw(splitting,n).
synw(splitting, ving).
synw(stimulate,v).
synw(stimulate, vp).
eynw(stimulated, ved).
synw(stimulated, ven).
synw(stimulates, vp).
synw(stimulating,n).
synw(stimulating, ving).
synw(stimulation, n).
synw(substitute,v).
synw(substitute, vp).
synw(substituted, ved).
synw(substituted, ven).
eynw(eubstitutes,vp).
eynw{eubstituting,n).
synw(substituting, ving).
```

```
synw(substitution, n).
synw{suppress, vp}.
evnw(suppress, V).
synw (suppressed, ved).
synw(suppressed, ven).
synw(suppresses, vp).
synw(suppressing,n).
synw(suppressing, ving).
synw(suppression, n ).
synw(tie,n).
synw(tie, v).
synw(tie, vp).
synw(tied, ved).
synw(tied, ven).
synw(ties,vp).
synw(transcribe, v).
synw(transcribe, vp).
synw(transcribed, ved).
synw(transcribed, ven).
aynw(transcribes, vp).
synw(transcribing,n).
synw(transcribing, ving).
synw(transcription.n).
synw(tying,n).
synw(tying, ving).
synw(ubiquitinization, n).
synw(ubiquitinize, v).
synw(ubiquitinize, vp).
synw(ubiquitinized, ved).
synw(ubiquitinized, ven).
synw (ubiquitinizes, vp).
synw (ubiquitinizing, n).
eynw (ubiquitinizing, ving).
synw (urge, n).
synw(urge, v).
synw (urge, vp).
synw (urged, ved).
synw (urged, ven).
synw (urges, vp) .
synw (urging, n).
synw (urging, ving) .
% the following are verbs connected with complexes
synw(form, v). .
```

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```
synw (form, vp).
synw(forms, vp).
synw(formed, ved).
synw(formed, ven).
synw (forming, n).
synw(formation, n).
synw(assemble,v).
aynw(assemble, vp).
synw(assembles, vp).
synw(assembled, ved).
synw(assembled, ven).
synw(assembling,n).
synw (assembly, n).
synw (dissassemble, v).
synw(dissassemble, vp).
synw(dissassembles, vp).
synw{diseassembled, ved}.
synw (dissassembled, ven).
synw(dispaseembling,n).
synw(diseaseembly,n).
synw(dissociate, v).
synw(dissociate, vp).
synw(dissociates, vp).
synw(dissociated, ved).
synw(dissociated, ven).
aynw (dissociating, n).
synw(dissociation,n).
synw(recruit, v).
synw(recruit, vp).
synw(recruits, vp).
synw(recruited, ved).
synw(recruited, ven).
synw{recruiting,n}.
synw {recruitment, n).
```

```
% lexsemact.pat
% revised March 17, 2000
             SEMANTIC LEXICON OF ACTIONS
For genomics - the grammar tests for semantic and syntactic cate
% separately for action type of categories; for substances the lex
% entries are the same as in the medical area
% action type phrases have two entries: a semantic entry and a syn
tactic entry
% This lexicon contains the semantic entries for words and phrases
% semp is a lexical entry for phrasal lexicon
% semp(+Word1,+Sem,+Wordlist,+Targetform,+Features)
% semp spacifies a semantic lexical definition for the genomics li
terature
% semp is equivalent to the predicate "phrase" in the medical area
% semp: Wordl is first word of phrase, Sem is semantic category
% semp: Wordlist is list of words in phrase, Targetform is output
% semp: Features is a list of 2 elements or the atom "def" represe
nting defaul
% samp: Features 1st element is rev or nrev meaning reversed or no
t reversed
% semp: Features 2nd element is a # specifying number of arguments
 for action
% semp: Features - def is equivalent to a list = [nrev,2]
% in case action has 1 argument, use [1,_]
%semw is a lexical entry for single word
% semw(+Word, +Sem, +Targetform, +Features)
% semw: the arguments are the same as for semp except there is no
Wordlist
*8*8*8
:- multifile (semp/5).
:- multifile (semw/4).
semp(account, cause, [account, for], cause, [def]).
semp(accounted, cause, [accounted, for], cause, [def]).
```

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```
semp(accounting, cause, [accounting, for], cause, [def]).
semp (accounts, cause, [accounts, for], cause, [def]).
semp(add, attach, [add, up], attach, [def)).
semp(added, attach, [added, up], attach, [def]).
semp(adds, attach, (adds, up), attach, (def)).
semp(are, cause, [are,a,means,of, producing),cause, [def]).
semp(are,cause,[are,due,to],cause,[2,rev]).
semp(as,cause,[as,a,result,of],cause,[2,rev]).
semp(attributable, rause, [attributable, to], rause, [2, rev]).
semp(attributed, cause, [attributed, to], cause, [2, rev]).
semp (based, cause, [based, on], cause, [2, rev]).
semp (based, cause, [based, upon], cause, [2, rev]).
semp(because, cause, [because, of], cause, [2, rev]).
semp(convey, signal, [conveys,a, signal], signal, [def]).
semp(conveyed, signal, [conveyed, a, signal], signal, {def}).
semp(conveying, signal, [conveying, a, signal], signal, [def]).
gemp(conveys, signal, [conveys,a, signal],signal, [def]).
semp(dissociate, release, [dissociate, from], release, [def]).
semp(dissociated, release, [dissociated, from], release, [def]).
semp{dissociates, release, [dissociates, from], release, [def]).
semp{dissociation, release, [dissociation, from], release, [def]).
semp(down, signal, [down, '-', regulate], signal, [def]).
regulates B
                   A --> B
semp(down, signal, [down, '-', regulated), signal, [def]).
                                                               A down
-requlates B
                    A --> B
semp(down, signal, [down, '-', regulates], signal, [def]).
                                                               A down
-regulates B
                     A --> B
semp(down, signal, [down, '-', regulation], signal, [def]).
                                                               A dow
                    A --> B
n-requiates B
semp(due, cause, [due, to, the, fact, that], cause, [2, rev]).
semp(due, cause, [due, to], cause, [2, rev]).
semp(form, attach, [form, complex], attach, [def]).
gemp(formation, attach, [formation, of, complex], attach, [def]).
semp(formed, attach, [formed, complex], attach, [def]).
semp(forms, attach, [forms, complex], attach, [def]).
semp(had, cause,[had,an,active,role,in],cause,[def]).
semp(has, cause,[has,an,active,role,in),cause,[def]).
semp(have, cause, [have, an, active, role, in], cause, [def]).
semp(is, cause, [is,a,means,of, producing], cause, [def] }.
semp(is, cause, [is, due, to], cause, (2, rev)).
semp(functions, inactivate, (functions, as, a, negative, regulator, of), i
nactivate, [def]).
semp(function, inactivate, [function, as, a, negative, regulator, of), ina
```

```
ctivate, [def] } .
semp(lead, cause, [lead, to], cause, [def]).
semp(lead, cause1, [lead, to], cause, [def]).
semp(leading, cause, [leading,to], cause, [def]).
semp(leading, cause, [leading, to], cause, [def]).
semp(leads, cause, [leads,to], cause,[def]).
semp(leads, cause1, (leads, to), cause, [def]).
semp(led, cause, [led, to], cause, [def]).
semp(may, cause, [may, be, responsible, for), cause, [def]).
semp(mediate, signal, {mediate, a, signal), signal, [def]).
                                                                 ВÀ
mediates a signal to B
semp(mediated, signal, [mediated, a, signal], signal, [def]).
A mediates a signal to B
semp(mediates, signal, [mediates, a, signal], signal, [def]).
A mediates a signal to B
semp(mediation, signal, [mediation.of, a, signal), signal, [def]).
    %A mediates a signal to B
semp(n, createbond, [n,'-',acetylate],'N-acetylate',[def]).
semp(n, createbond, [n,'-',acetylated],'N-acetylate', {def]}.
semp(n, createbond, [n.'-', acetylates], 'N-acetylate', [def]).
semp(n, createbond, [n,'-',acetylation],'N-acetylate',[def]).
semp{n, createbond, [n,'-',acylate],'N-acylate',[def]).
semp(n, createbond, [n,'-',acylated],'N-acylate', [def]).
semp(n, createbond, [n,'-',acylates],'N-acylate',[def]).
semp(n, createbond, {n,'-',acylation},'N-acylate', [def]).
semp(n, createbond, [n,'-',glycosylate],'N-glycosylate',[def]).
semp(n, createbond, [n,'-',glycosylated),'N-glycosylate',[def]).
semp(n, createbond, [n,'-',glycosylates],'N-glycosylate',[def]).
semp(n, createbond, [n,'-',qlycosylation],'N-glycosylate',[def]).
semp(n,breakhond,[n,'-',terminal,proteolysis],'n-terminal proteoly
sis',[def]).
semp(o, createbond, [o.'-'.glycosylate], '0-glycosylate', [def]).
semp(o, createbond, [o,'-',glycosylated], 'O-glycosylate',[def]).
semp(o, createbond, [o,'-',glycosylates], 'O-glycosylate', [def]).
semp(o, createbond, [o,'-',glycosylation], '0-glycosylate',[def]),
semp(only,time,[only,after],'only after',{2.rev]).
semp(proly1, createbond, [proly1,'-',4,'-',hydroxylate],
                   'prolyl-4-hydroxylate', [def]).
semp{proly1, createbond, [proly1, '-', 4, '-', hydroxylated],
                     'prolyl-4-hydroxylate', [def]).
semp(prolyl, createbond, [prolyl,'-',4,'-',hydroxylates],
               'prolyl-4-hydroxylate', [def]).
semp(prolyl, createbond, [prolyl,'-',4,'-',hydroxylation],
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'prolyl-4-hydroxylate', [def]}.
semp(result, cause, [result, from], cause, [2, rev]).
semp(result, cause, [result, in], cause, [def]).
semp (resulted, cause, (resulted, from), cause, (2, rev)).
semp{resulted, cause, {resulted, in}, cause, [def]).
semp(resulting, cause, (resulting, from), cause, (2, rev)).
semp(resulting, cause, [resulting, in], cause, [def]).
semp(results, cause, [results, from], cause, [2, rev]).
semp(results, cause, [results, in], cause, [def]).
semp(set, release, (set, free), release , [def]).
semp(set, release, [set, free], release .[def]).
semp(sets, release, [sets, free], release , [def]).
semp(setting, release, [setting, free], release , [def]).
semp(suppress, inactivate, [suppress, activity, of], inactivate, [
def)}.
semp(suppressed, inactivate, [suppressed, activity, of], inactivat
e. [def]).
semp(suppresses, inactivate, [suppresses, activity, of], inactivat
e, [def]).
semp(suppression, inactivate, [suppression, of, activity, of], inac
tivate, [def]).
eemp(switch, activate, [switch, on, the, activity, of], activate
, {def}}.
semp(switched, activate, (switched, on, the, activity, of),
vate, [def]).
semp(switches, activate, [switches, on, the, activity, of],
vate, [def]).
semp(up, signal, [up, '-', regulate], signal, [2, rev]). % A up-regul
ates B B --> A
semp(up, signal, [up, '-', regulated), signal, (2, rev)).
eemp(up, signal, [up, '-', regulates), signal, [2, rev]).
semp(up, signal, [up, '-', regulation], signal, [2, rev]).
semp(was, cause, [was, a, means, of, producing], cause, [def]).
Bemp(was,cause,[was,due,to],cause,(2,rev]).
semp(were, cause, [were,a, means, of, producing], cause, [def] }.
semp(were, cause, [were, due, to], cause, [2, rev]).
semw(acetylate, createbond, acetylate, [def]).
semw(acetylated, createbond, acetylate,[def]).
semw(acetylates, createbond, acetylate,[def]).
semw(acetylation, createbond, acetylate, [def]).
semw(activate, activate, activate, {def}).
semw(activated, activate, activate, (def)).
semw(activates, activate, activate, (def)).
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semw(activation, activate, activate, [def]).
semw(add, attach, attach, [def]).
semw(added, attach, attach, [def]).
semw(addition, attach,
                         attach. [def] }.
semw{adds, attach, attach, {def}}.
semw(after,time,after,[2,rev]).
                                    % temporal relations
semw(aggregate ,attach,attach,[def)).
semw(aggregated ,attach,attach,[def]).
semw(aggregates, attach, attach, [def]).
semw(aggregation ,attach,attach,[def]).
semw(arrest, inactivate, inactivate, [def]).
semw(arrested, inactivate, inactivate, [def]).
semw(arrests, inactivate, inactivate, [def]).
semw(associate, attach, attach, [def]).
semw (associated, attach, attach, [def]).
semw(associates, attach, attach, [def]).
semw(association, attach, attach, [def]).
semw(attach, attach, attach, [def]).
semw(attached ,attach,attach,[def]).
semw(attaches, attach, attach, [def]).
semw {attachment, attach, attach, [def] }.
semw (bind, attach, attach, [def]).
semw(binding, attach, attach, [def]).
semw(binds,attach,attach,[def]).
semw(block,inactivate,inactivate,[def]).
semw(blocked, inactivate, inactivate, [def]).
semw(blocking, inactivate, inactivate, [def]).
semw(blocks,inactivate,inactivate,[def]).
semw(bound, attach, attach, [def]).
semw(break, breakbond, 'break bond', [def]).
semw(breakage, breakbond,
                            'break bond', {def}).
semw(breaks, breakbond,
                          'break bond', [def]).
semw(broke, breakbond,
                         'break bond', (def)).
semw(broken, breakbond, 'break bond', [def]). % case without break
semw{catalyzation.promote.catalyze, [def]}.
eemw(catalyze,promote,catalyze, [def]).
semw(catalyzed,promote,catalyze,[def]).
semw(catalyzes, promote, catalyze, [def]).
semw(catalyzing,promote, catalyze,[def]).
semw(cause, cause, cause, [def]).
semw(caused, cause, cause, [def] ).
Bemw(causes, cause, cause, [def]).
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semw(cleavage, breakbond,
                            'break bond', [def]).
semw(cleave, breakbond,
                         'break bond', [def]).
semw(cleaved, breakbond,
                           'break bond', [def] }.
semw(cleaves, breakbond,
                          'break bond', [def] } .
semw(coimmunoprecipitate, attach, attach, [def]).
semw(coimmunoprecipitated ,attach,attach,[def]).
semw(coimmunoprecipitates, attach, attach, [def]).
semw{coimmunoprecipitation ,attach,attach,[def]).
semw(combination ,attach,attach,[def]).
semw(combine .attach.attach,[def]).
semw(combined ,attach,attach,[def]).
semw(combines, attach, attach, [Ref]).
semw(conjugate ,attach,attach, [def]).
semw(conjugated ,attach,attach,[def]).
semw(conjugates,
                  attach, attach, [def]).
semw(conjugation ,attach,attach, [def]).
semw(connect ,attach; attach, [def]).
semw(connected ,attach,attach,[def]).
semw(connection ,attach,attach,[def]).
semw(connects, attach, attach, [def]).
semw(constrain, inactivate, inactivate,[def]).
semw(constrained, inactivate, inactivate,[def]).
semw(constrains, inactivate, inactivate,[def]).
semw(constraint, inactivate, inactivate, [def]).
semw(coprecipitate, attach, attach, [def]).
semw(coprecipitated,attach,attach,[def]).
semw(coprecipitates, attach, attach, [def]).
semw(coprecipitation ,attach,attach,[def]).
semw(copurification ,attach,attach, [def]).
semw(copurified ,attach,attach, [def]).
semw(copurifies, attach, attach, [def]).
semw(copurify ,attach,attach,[def]).
semw(couple ,attach,attach,[def]),
semw(coupled, attach, attach, [def]).
semw(couples, attach, attach, [def]).
semw(cut, breakbond, 'break bond',[def]). % leave breakbond onl
semw(cuts, breakbond, 'break bond', [def]).
semw(deactivate, inactivate, inactivate, [def)).
semw(deactivated, inactivate, inactivate, [def]).
semw(deactivates, inactivate, inactivate,(def)).
semw(deactivation, inactivate, inactivate.[def]).
semw(death, process, death,[1]).
```

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semw(demethylate, breakbond, demethylate, [def]).
semw(demethylated, breakbond, demethylate,[def]).
semw(demethylates, breakbond, demethylate, [def]).
semw(demethylation, breakbond, demethylate,[def]).
semw(dephosphorylate, breakbond, dephosphorylate, [def]).
semw(dephosphorylated, breakbond, dephosphorylate, [def]). .
semw{dephosphorylates, breakbond,dephosphorylate,[def]).
gemw{dephosphorylation, breakbond,dephosphorylate,[def]].
semw(die, process, death,[1]).
semw (died, process, death, [1]).
semw(dies, process, death,[1]).
semw(disapsemble, release, release,[def]).
semw(disassembled, release, release, [def]).
semw(disassembles, release, release, [def]).
semw(disappembly, release, release, [def]).
semw(discharge, release, release, [def]).
semw(discharged, release, release, [def]).
semw(diecharges, release, release, [def]).
semw(disengage, release, release, [def]).
semw(disengaged, release, release, [def]).
eemw(disengagement, release, release, [def]).
semw(disengages, release, release,[def]).
semw(divide, breakbond, 'break bond', [def]).
semw(divided, breakbond, 'break bond', [def]).
semw(divides, breakbond, 'break bond', [def]].
semw(division, breakbond, 'break bond', [def]).
semw(dying, process, death, [1]).
semw (enhance, promote, promote, [def]).
semw(enhanced, promote, promote, [def]).
semw(enhancement, promote, promote, [def)).
semw(enhances, promote, promote, [def]).
semw(enhancing,promote,promote, [def]).
semw(express, generate, express, [def]). % can have either 1 or 2 ar
gumenca
semw (expressed, generate, express, [def]).
semw(expresses, generate.express,[def]).
semw(expressing, generate,express,(def)).
semw(expression,generate,express,[def]).
semw(generate,generate,generate,[def]).
semw(qenerated.generate,generate,[def]).
semw(generates,generate,generate,[def]).
semw(generating,generate,generate,[def]).
semw(generation,generate,generate,[def]).
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semw(hew, breakbond, 'break bond', [def]).
semw(hewed, breakbond, 'break bond', [def]).
semw(hews, breakbond, 'break bond', [def]).
semw(hinder, inactivate, inactivate, [def]).
semw(hindered, inactivate, inactivate, [def]).
semw(hinders, inactivate, inactivate, [def]).
semw(hindrance, inactivate, inactivate, [def]).
semw(inactivate, inactivate, inactivate, [def]).
semw(inactivated, inactivate, inactivate, [def]).
semw(inactivates, inactivate, inactivate, [def]).
semw(inactivation, inactivate, inactivate,[def]).
semw(incite, activate, activate,[def]).
semw(incited, activate, activate, [def]).
semw(incitement, activate, activate, [def]).
gemw(incites, activate, activate,[def]).
semw(induce, activate, activate, [def]).
semw(induced, activate, activate,[def]).
semw(induces, activate, activate, [def]).
semw(induction, activate, activate, [def]).
semw(influence, activate, activate, [def]).
semw(influenced, activate, activate, [def]).
eemw{influences, activate, activate,[def]].
eemw(influencing, activate, activate,[def]).
eemw(inhibit, inactivate, inactivate,[def]).
Bemw{inhibited, inactivate, inactivate, [def]).
semw(inhibition, inactivate, inactivate, [def]).
semw(inhibits, inactivate, inactivate,[def]).
semw(initiate, activate, activate, [def]).
semw(initiated, activate, activate, [def]).
semw(initiates, activate, activate, [def]).
semw(initiattion, activate, activate, [def]).
semw(instigate, activate, activate,[def]).
semw(instigated, activate, activate,[def]).
semw(instigates, activate, activate,[def]).
semw(instigation, activate, activate,[def]).
semw(interact, interact, interact,[def]).
semw(interacted, interact, interact, [def]).
semw(interaction, interact, interact, [def]).
semw(interactions, interact, interact, [def]).
semw(interacts, react, interact, [def]).
semw(join ,attach,attach,[def]).
semw(joined ,attach, attach,[def]).
semw(joining, attach, attach, [def]).
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semw(joins, attach, attach, [def]).
semw(juncture, attach, attach, [def]).
semw(liberate, release, release, [def]).
semw(liberated, release, release, [def]).
semw(liberates, release, release, [def]).
semw(liberation, release, release, [def]).
gemw{limit, inactivate, inactivate, [def]).
memw{limitation, inactivate, inactivate,[def]}.
semw(limited, inactivate, inactivate, (def)).
semw(limits, inactivate, inactivate, [def]).
semw(link,attach,attach,[def]).
semw(linked, attach, attach, [def)).
semw(linking, attach, attach, (def)).
semw(links, attach, attach, [def]).
semw{mediate, promote, promote, [def]).
semw(mediated, promote, promote, [def]).
semw(mediates, promote, promote, [def]).
semw(mediation, promote, promote, [def]).
serw(methylate, createbond, methylate, [def]).
semw(methylated, createbond, methylate,[def]).
semw(methylates, createbond, methylate, [def]).
semw (methylation, createbond, methylate, [def]).
semw (modification, modify, modify, [def]).
semw (modified, modify, modify, [def]).
semw (modifies, modify, modify, [def]).
semw (modify, modify, modify, [def]).
semw (modifying, modify, modify, [def]).
semw (mutate, modify, mutate, [1]).
semw (mutsted, modify, mutate, [1]).
semw (mutates, modify, mutate, [1]).
semw(mutating, modify, mutate, [1]).
semw(mutation, modify, mutate, [1]).
semw(overexpressed, generate, overexpress, [def]).
semw(overexpresses, generate, overexpress, [def]).
semw(overexpressing, generate, overexpress, [def]).
semw(overexpress, generate, express.[def]).
semw(overexpression,generate,overexpress,[def]).
semw(pair, attach, attach, [def]).
semw(paired, attach, attach, [def]).
semw(pairing, attach, attach, [def]).
semw(pairs, attach, attach, [def]).
semw(phosphorylate, createbond, phosphorylate, [def]).
semw(phosphorylated, createbond, phosphorylate, [def]).
```

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semw(phosphorylates, createbond, phosphorylate,[def]).
semw{phosphorylation, createbond, phosphorylate,{def}).
semw(prec de, cause, cause,[def]).
semw(preceded, cause, cause, [def)).
semw(precedes, cause, cause, [def]).
semw(preceding, cause, cause, [def]).
semw (promote, promote, promote, [def]).
semw (promoted, promote, promote, [def]).
semw (promotes, promote, promote, [def]).
Bemw(promotion, promote, promote, [def]).
semw(prompt, activate, activate, [def]).
semw(prompted, activate, activate, [def]).
semw(prompting, activate, activate, [def]).
semw(prompts, activate, activate, [def]).
semw(react, react, react,[def]).
semw{reacted, react, react, [def]}.
semw(reaction, react, react, [def]).
semw(reactions, react, react, [def]).
semw{reacts, react, react,[def]).
semw(regulate, signal, signal, [def]).
semw(regulated, signal, signal, [def]).
                                              & B is regulated by
semw(regulates, signal, signal, [def]).
semw(regulation, signal, signal, [def]).
semw(release, release, release, [def]).
semw(released, release, release, [def]).
semw(releases, release, release,[def]).
semw(removal, breakbond, 'break bond ', [def]).
semw(remove, breakbond, 'break bond ', [def]).
semw(remove, breakbond, 'break bond ', [def]).
semw(removes, breakbond, 'break bond ', [def]).
semw(replace, substitute, substitute, [def]),
semw(replaced, substitute, substitute, [def]).
semw(replacement,
                    substitute, substitute, [def]).
semw(replaces, substitute, substitute, [def]).
semw(repress, inactivate, inactivate, [def]).
semw(repressed, inactivate, inactivate, [def]).
semw(represses, inactivate, inactivate, [def]).
semw(repression, inactivate, inactivate,[def]).
semw(require, cause, cause, [2, rev]).
semw(required, cause, cause, [2, rev] ).
semw(requirement, cause, cause, [2, rev]).
semw(requires, cause, cause, (2, rev) ).
```

```
semw(requiring, cause, cause, (2, rev) ). .
 semw(restrain, inactivate, inactivate, [def]).
 semw(restrained, inactivate, inactivate, [def]).
 semw(restrains, inactivate, inactivate, (def)).
 semw(restraint, inactivate, inactivate, [def]).
 semw(sensitization, activate, activate, [def]).
 semw(sensitize, activate, activate, [def]).
 semw(sensitized, activate, activate,[def]).
 semw(sensitizes, activate, activate,[def]).
 semw(separate, breakbond, 'break bond', [def]).
 semw(separated, breakbond,
                             'break bond', [def]).
 semw(separates, breakbond, 'break bond', [def]).
 semw(separation, breakbond, 'break bond', [def]).
                         'break bond', [def] } .
 semw(sever, breakbond,
                              'break bond', [def] } .
 semw(severance, breakbond,
                            'break bond', [def] }.
 semw(severed, breakbond,
 semw(severs, breakbond, 'break bond', [def]).
 semw(signal, signal, signal, [def]).
 semw(signaled, signal, signal, [def]).
 semw(signaling, signal, signal, [def]).
 semw(signals, signal, signal, [def]).
semw(split, breakbond, 'break bond', [def]).
 semw(splits, breakbond, 'break bond', [def]).
 semw(splitting, breakbond, 'break bond', [def]).
 semw(stimulate, activate, activate, [def]).
 semw(stimulated, activate, activate, [def]).
 semw(stimulates, activate, activate, [def]).
 semw(stimulation, activate, activate, [def]).
 semw(aubstitute, substitute, substitute,[def]).
 semw(substituted, substitute, substitute, [def]).
 aemw(Substitutes, substitute, substitute, [def]).
 semw(substitution, substitute, substitute, [def]).
 semw(suppress, inactivate, inactivate, [def]).
 semw(suppressed, inactivate, inactivate, [def]).
 semw(suppresses, inactivate, inactivate, [def]).
 semw(suppression, inactivate, inactivate,[def]).
 semw(tie.attach.attach.[def]).
 semw(tied, attach, attach, [def]).
 semw(ties, attach, attach, [def]).
 śemw(transcribe.generate.transcribe.[def]).
 semw(transcribed,generate,transcribe,[def]).
 semw(transcribes,generate,transcribe,[def]).
 semw(transcribing,generate,transcribe,[def]).
```

```
semw(transcription, generate, transcribe, [def]).
semw(ubiquitinize, createbond, ubiquitinize, {def]).
semw(ubiquitinize, createbond, ubiquitinize,[def]).
semw(ubiquitinized, createbond, ubiquitinize, [def]).
semw(ubiquitinizes, createbond, ubiquitinize,[def]).
semw(urge, activate, activate, [def]).
pemw(orge, activate, activate,[def]).
semw(urged, activate, activate,[def]).
semw(urges, activate, activate, [def]).
semw(urging, activate, activate, (def)).
semw(form,attach,attach,[def]).
semw(forms, attach, attach, [def)).
semw(formed, attach, attach, [def]).
semw(forming, attach, attach, {def}).
semw (formation, attach, attach, [def]).
semw(assemble, attach, attach, [def]).
semw (assembles, attach, attach, [def]).
semw(assembled, attach, attach, [def]).
semw (assembling, attach, attach, [def]).
semw (assembly, attach, attach, [def]).
semw (dissassemble, release, release, [def]).
semw(dissassembles,release,release,[def)).
semw(dissassembled, release, release, [def)).
semw(dissassembling, release, release, (def]).
semw(dissassembly, release, release, [def]).
semw(dissociate, release, release, [def]).
semw(dissociates, release, release, [def]).
semw(dissociated, release, release, [def]).
semw(dissociating, release, release, [def]).
semw(dissociation, release, release, [def]).
semw(recruit, attach, attach, [def]).
semw(recruits, attach, attach, [def]).
semw (recruited, attach, attach, [def])...
semw(recruiting,attach,attach,[def]).
semw (recruitment, attach, attach, [def]).
```

```
t edited Genome grammer - adapted from MedLEE's grammar for use with MedLEE
% this is to be used along with the genomics lexicon of substances, actions.
   and relations.
t revised March 16, April 5, 2000
* adjusted for tagged input
:- multifile(wdef/3).
:- multifile(phrase/5).
ŧ
      Written by Carol Friedman for the MadLEE System
R
      Queens College of the City University of New York
无毛毛密介色写示于同分表多句的介质感染力主要并已由有它的介质实质的介质实现有主要的变更的分介的企业主要企业介质的介质主要介质的原则活作着用电影的介质方式
Y Highest Level Predicate - sem gent - lst arg. is target structure

    2nd arg. is a list of words in sentence

                                   - 3rd arg, is '[]'
t Target structure: a frame or set of connected frames:
          the frame describes an action or several related actions;
          an action frame is a list consisting of the symbol 'action'
ŧ
          followed by the code for the action and arguments.
          The arguments are either substances or actions;
          tach substance slot consists of the name of the type of
          substance followed by the value for the substance;
          the substance slot may contain slots for several substances.
* Examples:
* Blocking of il-2 gene transcription by activated rapl.
t (action, inactivate, (protein, Rapl, [state, active]),
                    {action, transcribe, [x], [gene, interleuxin-2]]}
* The adapter protein crkl was associated with both phosphorylated cbl and the *
t guanidine nucleotide-releasing factor clg.
* [action,attach, [protein,CrkL],
                [relation, and, [protein, Cbl, [state, phosphorylated]],
                            [protein, quantitine nucleotide-releasing factor C3G,
                                                 [state,phosphorylated)]]] t
fail an unknown predicate
-- unknown(_,fail).
:- op(900, fy, [not,once]). & same priority and type as \+
:- op(700, xfx, [\=,-=]).
                            t same priority and type as = or --
a snoop is generally used to find input string when using a DCG
       the input string is used for constraints
snoop(A,B,A,B).
sem_sent(P,gemlist,X) -->
       {assert {addstotal (0) ) },
       sem paras (P. Semlist, X).
sem_parse(Target,Semlist) -->
       sem_patterns(P, Semlist).
sem paras(Target, Semlist, X) -->
       sem_patterns (P.Semlist) .
       sem_endornot {P, Target, X}.
sem_parse{[failure],_,X,_,_} :-
       addstotal (X).
sem_endornot(P,P,X) --> % P is target if there is an endmark
```

Appendix D

```
eem endmark.
       {addatotal(X)}. % X is number of times reached endmark
sem_endornot(_,_,_,_) :- % did not reach endmark; update count and fail
       uptotal, fail,
eem_endornot(_,[failure],X,_,_) :-
       addstotal(X), * X is number of times reached
       x = 50.
* Finding potterns
sem patterns (F, Semlist) -->
       pattern(F1,Semlist),
       morepattern(R, P2, Semlist), % connected patterns
       (getrelation(R,F1,F2,F)).
* The action pattern types are: pattern, nounactionpatt, actpatt. and 🔸
* nounactpatt.

    pattern --> actionarg(Al)

             active or passive verb
            actionarg(A2).
* pattern --> nounactionpatt.
* pattern --> actpatt.
* pattern is saved in a symbol table (st); check for success/failure lst
* Case where pattern is in st and has been successful
pattern(Pmt,_) --> checkst(pattern,_,s,Fmt).
t Case where pattern is in at as a failure.
pattern(_,_) --> checkst(pattern,_,f,_}, {i, fail).
& pattern 5: an action pattern with a nominal varb
* P:1 cleavage by zvad.
* apoptosis-induced cleavage of P62 by zDEVD.
pattern(F,Semlist) -->
    snoop (S0, S0),
  { \+ checkst(pattern,5,_,_,S0,_),
    actionchk(Semlist) };
    nounactionpatt(F);
    элоор (8, 2),
  ( addst (pattern, 5, s, F, 80, 8)
t pattern 1: an action/substance acts on an action/substance
the activation of rapi inhibits the expression of 11-2
4 rapl functions as a negative regulator of tor-mediated il-2 gene
4 transcription.
                     snoop(80,80), & 30 is the input string
pattern(F,Semlist) -->
  { \+ checkst(pattern, 1, _, _, S0, _).
    actionchk(Semlist),
    connectchk(Semlist) ),
    actionarg[Al),
```

```
connectact (Sem, [v, vp, ved], Target, Features),
     actionarg(A2),
     snoop(S,S), tending sentence list
   { member(def, Features),
     modlist([A1,A2,Site],Mods);
     member (rev. Features),
     modlist((A2, A1, 6ite), Mode)).
     frame (?, action, Target, Mods),
     addst (pattern, 1, s, P, So, S)
pattern 2: an action/substance was acted on by an action/substance
t The aggregation of bad was suppressed.
t The aggregation of bad was suppressed by the phosphorylation of jnk.
% Grb2 was associated with Cbl.
* Apoptosis-associated cleavage of endogenous PSI was blocked by the
* treatment with zVAD.
pattern(f, Semlist) -->
     snoop($0,50), $ 60 is the input string
    ( \+ checket(pattern, 2, _, _, 80, _).
      actionchk(Semliat),
      connectchk(Semlist) ),
      actionary (A2),
      sem beterm{_},
                        * was
      connectact (Sem, [ven] , Target, Features) , tactivated
      opthyarg(Al),
   snoop(8,3), tending sentence list
{ (member(def, Features),
      modlist([Al,A2,Site),Mods);
      member(rsv.Features),
      modlist([A2,A1,Site],Mods)},
      frame (F, action, Target, Mode),
      addsr(pattern, 2, s, P, SO, S)
   }.
t pattern 3: an action/substance acted on an action/substance
t bad induced phosphorylation of fyn.
ter and cd28-mediated il-2 transcription.
pattern(F.Semlist) -->
     snoop ($0,50),
   { \+ checkst(pattern, 3,_,_,s0,_),
     actionchk(Semlist),
     connectchk(Semlist) },
     actionary(Al),
                      * substance or basic action
   t optdash,
     connectacts (fom, [vp, ven, ved], Target, Features), ' & 'activated'
   & optof,
     actionarg(A2), & had pattern here
     encop(S,S),
  { {member(def, Features),
     modlist([A1,A2,Site],Mods);
     member(rev.Features),
     modlist([A2,A1,Site],Mods)),
     frame (F, action, Target, Mods),
     addst(pattern, 3, s, F, SO, 6)
  1:
```

```
t pattern 4: a simple action pattern with an active verb.
  t Activated Raf-1 phosphorylates MEK-1.
  pattern(P,Semlist) -->
       snoop (90, 60),
       tcheck that sentence has an action word/phrase
     { \+ checkst(pattern, 4,__, so,_).
       actionchk(Semlist) },
       actpatt (F).
       snoop (S, S),
     { addst(pattern, 4, s, F, SO, S)
  t no more patterns - save failure
 pattern(_,_) --> addst[pattern,0,f,_), {!, fail}.
   sem_morepattern(-Rel,-P,+Semlist,+80,+5):
 4
          Rel is a relation and its value frame;
 *
          P is the remaining patterns, Semlist is the list of semantic classes
          in sentence
 * if have a series of ','s, use the relation "and" or "or" if in the mest
 t and make that the relation
morepattern(R,F,Semlist) -->
                                   trelation and modifiers
          sem_relation(R1,Mod1),
          cem_patterns(F.Samlist),
          (Conj2 = end; Conj2 = or), frame(R1,rel,',',_), % R1 relation frame
             frame (R, rel, Conj2, ) & value of relation is Conj2
            R1 \= (), t where do Type, Value and Mods2 come from? frame(R1, Type, Value, Mod2), t get components of original relation
            mergemods (Mod1, Mod2, Mods),
            \{ Mods = (), frame(R, rel, Value, ()), !; 
              fframs (R. rel, [Value | Mods], []) * make it rel connector with rel mod
              R - [rel, [Value | Mode]]
            )
          1.
 % no more findings
 morepettern([],[],_,S,S).
 t actionary is the argument of pattern
 * actionary is either a substance or a basic action
 t actionary is saved in a symbol table (at); check for success/failure lat
 Case where actioners is in st and have been successful
 actionarg(A) --> checkst(actionarg,_,s,A).
 t Case where actionary is in st as a failure.
 actionarg(_) --> checkst(actionarg,__f;_), (1, fail).
 * actionarg 1: a substance or substances
 Rapl, active Rapl, Cbl and Crkl
 actionary(A) --> snoop(S0,S0), 4 S0 is the input string
                { \* checkst(actionarg,1,_,_,SD,_)},
                  substances(A),
                  snoop(E,S),
                { addst(actionarg, 1, 5, A, SO,S) }.
```

```
% actionarg 2: a process like apoptosis, or a disease
actionarg(A) --> snoop(SO,SO), t SO is the input string
              ( \+ checkst(actionarg, 2, _, _, 80, _)),
                processpatt(A),
                , (2,2) goons
              { addst(actionarg,2,9,A,S0,S)
   }.
* actionarg 3: a nominal action pattern
% Stoposide-induced apoptosis.
t Stoposide-induced PSI cleavage by zVAD.
actionarg(A) --> snoop($0,50). t SO is the input string
              ( \+ checkst(actionarg, 3, _, _, S0, _)),
                nounactionpatt(A),
                ancop (6,8).
                 (addst (actionarg, 3, s, A, S0.S)
% actionary 4: the object of the nominal action is an actionary
* Blocking of IL-2 Gene transcription by activated rapl.
actionarg(A) --> encop(SO,SO), % SO is the input string
                 { \+ checkst(actionarg, 4 ,__,_, 50,_) },
                   action(Sem, [n, ving), Target, Features),
                    (of),
                    actionary (Al),
                    optbyagent (A2),
                    snoop (S,S),
                 { (member{def, Peatures),
                    modlist([A1,A2],Mods);
                    member (rev. Features),
                   modlist([A2,A1],Mods)),
                    frame(A, action, Target, Mods),
                   addst(actionarg, 4, s, A, SO, S)
     ).
t no more actionary - save failure .
actionary() --> addst(actionary,0,f,_), {1, fail}.
% nounactionpatt is a nominal action pattern which allows for left and right
* modifiers
11-2 gene transcription mediated by ter and cd28 was inhibited by rapl.
% Activated rapl functions as a negative regulator of tor and cd-28-mediated
il_2 transcription.
t nounactionpatt is saved in a symbol table (st); theck for success/failure let
t Case where nounactionpett is in st and has been successful
nounactionpatt(A) --> checkst(nounactionpatt,_,s,A).
* Case where nounsction patt is in at as a failure.
nounactionpatt(_) --> checkst(nounactionpatt,_,f,_), {1, fail}.
                                        % SO is the input string
nounactionpatt(P) --> snoop(S0,S0).
                     { \+ checkst {nownactionpatt,1 ,_,_,SD,_)},
                       actionImod [L,Symi),
                       nounactionumit(A).
                       actionsmod(R, Syn2),
```

```
encop (5,8).
                     { (Syn1 = ved, append(R, {A), RA),
                        append(L, RA, P);
                        6ynl = ving, append(R, [A], RA).
                        L = [action, Verb, Object],
                        modlist (RA, Object, Mods).
                        frame(P, action, Verb, Mods) |,
                        addst(nounactionpatt,1,8,P,50,S1 }.
 * no more nounactionpatt - save failure
nounactionpatt(_) --> addet(nounactionpatt,0,f,_1, (:, fail).
 the central unit of the nounactionpath is a nounactpath or a process
nounactionumit(A) --> nounactpatt(A).
nounactionumit(A) --> process(A).
& left modifiers of nounactpatt
% Evad-inhibited cleavage pf Psi
actionlmod(L, ved) --> substances(S),
                       optdaah,
                       action (Sem, (ved), Target, Peatures ),
                     { frame(L, action, Target, (S)) }.
* apoptosis induced cleavage of ps2
action1mod(L,ved) --> process(9),
                       optdash,
                       action (Sem. [ved], Target. Features ),
                     [ frame{L, action, Target, [S]} }.
 & apoptosis causing cleavage of Psl by Evad.
 % need to invert the order of nounactpatt and action1mod
action1mod(L, ving) --> processobject(A), % process or nownacpatt,
                        action(Sem, [ving], Target, Features).
                      { frame(L,action, Target.A) }.
actionlmod([],_) --> [].
 actionrmod(R, ved) --> action(Sem, [ved), Target, Features).
                       byagent (A), t may have to add ving to action rmod
                    { frame (R, action, Sem, A) }.
actionrmod({[],_] --> [].
* actpatt parses a simple action between substances expressed by an active verb
% actpart is saved in a symbol table (st); check for success/failure % % lat
& Case where actpart is in st and has been successful
actpath(F) --> checket(actpath,_,s,F).
* Case where actpatt is in st as a failure.
actpatt(_) --> checkst(actpatt,_,f,_), {1, fail}.
* actpatt 1: substance acts on substance
 PDK1 phosphorylates prosek at Thr229
 actpatt(F) -->
     snoop(80,$0), % 80 is the input string
   { \+ checkst(actpatt,1 ,_,_,50,_)),
```

```
substances (Al) .
    sem whichrel,
                       % opt 'that'
    action (Semplass, (vp, ved), Target, Features),
    propopt, 3 added propopt to allow action 'to' and 'with' substance
    substances (A2),
    siteinfo(Site),
    Bnoop (S.S).
  { (member(def, Features),
    modlist([Al,A2,Site],Mode);
    member (rev. Peatures),
    modlist((A2, A1, Site], Mods)).
    frame (F, action, Target, Mods),
    eddst(actpatt,1 ,s,F,SD,S)
% acpatt 2:
& Substance was bound by Substance
& Substance was associated to substance.
& F can give either first or second place to the second argument;
t a byagent gets first position; prepagent gets second.
t Phosphorylated Fyn was associated with Cbl.
actpatt(F) ·->
    snoop(80,80), & SD is the input string
   \+ checkst (actpatt, 2, _, _, 60, _) }.
    aubstances(A1),
    sem_beterm(_),
    action (Semclass, [ven] , Target, Features) ,
    opthyorprepagent (Position, A2),
    snoop($,$),
 { (member{def, Features),
   (Position=second, modlist([Al,A2,Sits],Mods);
    Position= first, modlist([AZ,Al,Site),Mode));
    member (rev. Features) .
   (Position-second, modlist([A2,A1,Site],Mods);
   Position= first, modlist([Al,A2,Site],Modx))},
   frame (F. action, Target, Mods),
    addst (actpatt, 2, e, F, SD, S)
 1.
* no more actpatt - save failure
actpatt() --> addst(actpatt,0,f, ), {!, fail).
* nounactpatt parage a simple action between substances expressed by a nominal
* verb
t nounactpatt is saved in a symbol table (st); chack for success/failure 1st
t Case where nounactpatt is in st and have been successful
nounactpatt(Fmt) --> checkst(nounactpatt, ,s,Fmt).
Lese where nounactpatt is in st as a failure.
nounactpatt(_) --> checket(nounactpatt,_,f,_), {!, fail}.
* nounactpatt 1:
* Jok phosphorylation of Had
nounautpatt(P) -->
    snoop(S0,S0), % S0 is the input string
```

```
{ \* checkst(nounactpatt,1,_._,50,_) },
    substances (Al),
    {aminoacidtest(A1)}.
    optdaga,
    action(Samclass, [q], Target, Features),
    ofobject (A2),
    siteinfo($ite),
    snoop (S,S),
   { (member (def, Features) ,
     modlist([A1,A2,Site],Mods);
     member (rev, Features),
     modlist([A2,A1,Site],Mods)),
     frame (P, action, Target, Model,
     addst (nounactpatt, 1, s, P, S0, S)
   }.
% nounactpatt 2: the binding of substance and substance
t association of Pyn and Ch1.
the reason for having this as a separate pattern is to
t prevent 'Fym and Cbl' from being persed together as substances
nounactpatt(F) -->
    snoop(S0,S0), % 60 is the input string
 { \+ checkst(nounactpatt,2 ,_,_,90,_) ),
    action (attach, [ving, n], Target, Features),
    ofobject1(A1),
    andobject (A2),
 Y siteinfo(Site),
    snoop(S,S),
 { modlist([A1,A2,Site],Mods),
    frame (F, action, Target, Mods),
    addet (nounactpatt, 2, s, F, S0, S)
   Ì.
% nounactpatt 3:
t The cleavage of protein by substance.
* Association of phosphorylated Byn with Cbl
tyrosine phosphorylation of Cbl by kinase
t optbyorprepagent determines the order of arguments; byagent is placed first;
t prepagent is placed second
nounactpatt(F) -->
   snoop(S0,S0), * SO is the input string
    { \+ checkst(nounactpatt, 1 , _, _, so, _) },
    actionof(F).
    encop (5,9),
  { addst {nounactpatt,3 ,e,F,S0,S) }.
actionof(F) -->
    siteinfo(Site).
    action (Semclass, [ving, n], Target, Features),
    optofobject (A1),
    opthyorprepagent (Position, AZ),
    snoop(8,5),
  { (member {def, Features).
    (Position-second, modlist([A1,A2,Site],Mods);
     Position= first, modlist([A2,A1,Site],Mode));
     member (rev. Features).
```

```
{Position-second, modlist([AZ,Al,Site],Mods);
     Position= first, modlist([A1,A2,Site],Mode))),
     frame (F, action, Target, Mods)
  ].
% noumactpatt 4:
t Fyn association with Cbl.
nounactpatt(P) -->
    snoop (SO.SO), & SD is the input string
  { \* checkst(nounactpatt,4,_,_,SD,_) },
    substances (A1) .
    action (Semplass, (ving.n), Target, Features).
    withobject (A2),
  % siteinfo(Site),
    encop (S,S),
 { modlist([Al,A2,Site],Nods),
    frame (F, action, Target, Mode) .
    addst (nounactpatt, 4, s, P, SO, S)
 }.
aminoacidtest(X) :- X \= [aminoacid]_].
* nounactpatt 5:
% IL-2 gene transcription
* Chl phosphorylation [by substance or action]
nounactpatt(F) -->
    encop($0,90), & SD is the input string
    \+ checkst(nounactpatt,5 ,__, 50,_) },
    substances (AZ),
    optdash.
    action (Semclass, (n), Target, Features),
    optbyagent(Al),
 siteinfo(Site),
    encop (8.8),
 { (member (def, Features),
    modlist([Al,A2,Site],Mods);
    member (rev.Features),
    modlist([A2,A1,Site],Mode)),
    frame (P, action, Target, Mode),
    addet (nounactpatt, 5 , s, F, SO, S)
 }.
& nounactpatt 6:
* fyn-col association.
nounactpatt(F) -->
    snoop($0,50), & SO is the input string
    \+ checkst(nounactpatt.6 , _ , _ , S0, _ ) ),
   'substances (A1) ,
    optdash,
    substances (A2),
    action (Semclass, [n, ving) , Target, Features) ,
 t siteinfo(6its).
    encop (8,8),
  { modlist([A1,A2,Site],Mode),
    frame (F, action, Target, Mode),
    addst (nounactpatt, 6, 8, F, S0, SI
  }.
```

```
% nounactpatt 7:
t Col phosphorylated by fyn.
nounactpatt(F) -->
    ancop($0,$0), % $0 is the input string
    { \+ checkst(nounactpatt,7 ,_,_,50,_)},
    substances (A1) .
    action(Semclass, [ven], Target, Features),
    [by).
    substances (A2),
 v siteinfo($1te).
    ancop($,$).
 ŧ
             { (member (def, Peatures) ,
    { modlist([A2,A1,Site],Mode],
             member (rev. Peatures),
             modlist([A1, A2, Site], Mods)),
      frame (F, action, Target, Mods),
      addat (nounactpatt, 7, s, F, 50, 6)
    ١.
* no more nounactpatt - save failure
nounactpatt(_) --> addst(nounactpatt(0,f, ), {(, fail).
connectact (Sem, Syn, Target, Features) -->
      action (Sem, Syn, Target, Peatures),
     (member(Sem, [cause, causel, activate, inactivate, signal, substitute, promote])).
connectacts (Sem, Syn, Target, Features) -->
      connectact (Sem, Syn, Target, Features) .
* aminoacid like tyrosine : ex.: tyrosine Cbl phosphorylation
% at position 201 Thr
siteinfo(S) --> aminoacid(A),
                  {frame(S, site, (A), ())} .
aiteinfo(8)
                 Bitepreps, % 'in', 'at'
                position(S).
siteinfo([)) --> [].
sitepreps
              --> prepterm(in,_).
sitepreps
              --> prepterm{at,_}.
position(8) --> (position),
                sem_integerterm(I);
                { frame(S, sits, I, ()) }.
* The definitions of actions refer to the lexicons lexagnact.pl and lexagnact.pl
Sem is the semantic class; Syn is the syntactic class
F is the target
t oneaction was added for use with moreaction to allow parsing of conjoined
* actions
ontaction (activate, Syn, F, Ftatures)
                                        --> activateterm(Syn,F,Fcatures), { 1}.
oneaction(attach, Syn, F. Features)
                                        --> attachterm(Syn, F, Features), {|}.
oneaction(breakbond, Syn, F, Features)
                                        --> breakbondterm(Syn, F, Features), {!}.
```

```
oneaction(creatchond, Syn, F, Features)
                                         --> createbondterm(Syn, P, Features), (1).
oneaction (inactivate, Syn, F. Features)
                                         --> inactivateterm(Syn, P. Features), {!}.
                                         --> reactterm(Syn, F, Features), (!).
oneaction (react, Sym, F, Features)
                                          --> releaseterm(Syn, F, Features), (!).
oneaction(release, Gyn, F. Features)
oneaction(signal, Sym, F, Features)
                                         --> signalterm(Syn, P, Features). {!}.
                                         --> substituteterm(Syn, F, Features), {!}.
oneaction(substitute, Syn, F, Features)
                                         --> transcribeterm(Syn, F, Features), {! ).
oneaction(transcribe, Syn, F, Features)
                                         --> promoteterm(Sym,F,Features),(!).
oneaction(promote, Syn, P, Peatures)
oneaction (generate, Syn, F, Features)
                                         --> generateterm(Syn, P, Features), {!}.
                                           causeterm(Syn, P, Features), (!).
oneschion(cause, Syn, P. Features)
action(activate, Syn, F, Features)
                                      --> activateterm(Syn, Al, Paatures),
                             moreaction(Conj, Args),
                            {Conj - [],F =A1;
                            Conj\=[], mergemods([[action,Al)],Args,Actions),
                            frame (F1, relation, Conj, Actions), F - [F1] }.
action(attach, Syn, F, Peatures)
                                      --> attachterm(Syn,A1 [Features],
                            moreaction(Conj,Args),
                            \{Conj = \{\}, F -AL;
                            Conj\w(], mergemods{[[action, A1]], Args, Actions},
                            frame (F1, relation, Conj, Actions), F = [F1] ).
                                     --> breakbondterm(Syn,F,Features),
action(breakbond, Sym, F, Features)
                            moreaction(Conj,Args),
                            {Conj = {},F =A1;
                            Conj\=[], mergemods([[action,Al]],Args,Actions),
                            frame (F1, relation, Conj, Actions), F + [F1]}.
action(creatchond, Syn, F. Features) --> creatsbondterm(Syn, F. Features),
                            moreaction (Conj. Args),
                            \{Conj = [], F = A1;
                            Conj \= [], mergemods ( [[action, Al]], Args, Actions),
                            frame (F1, relation, Conj, Actions), F = [F1]}.
sction(inactivate,Syn,F,Features) --> inactivateterm(Syn,F,Features),
                            moreaction(Conj,Arga),
                            {Conj = [],F =A1;
                            Cond \=[], mergemods([[action, Al]], Args, Actions),
                            frame(F1, relation, Conj, Actions), F = [F1] ].
                                      --> reactterm(Sym, F, Features),
action(react, Sym, F, Features)
                            moreaction(Conj,Args),
                            (Conj - [], F = A1;
                            Conj = [], mergemode { [[action, Al]], Args, Actions),
                            frame [F1, relation, Conj, Actions], F - [F1]}.
action(release, Syn, F, Features)
                                     --> releaseterm(Syn, P, Fratures),
                            moreaction (Conj. Args).
                            \{Conf = [], F = A1;
                            Conj\=[]; margemods([[action,A1]],Args,Actions),
                            frame (Fi, relation, Conj, Actions), F - [F1] ).
                                     --> signalterm(Syn,F,Features),
action {signal, Syn, F, Features}
                            moreaction(Conj, Args),
                            \{Conj = [], F = A1;
                            Conj \= (), mergemode([(action, Al]), Args, Actions),
                            frame (F1, relation, Conj, Actions), F - [F1]).
action(substitute, Sym, 8, Features) --> substituteterm(Sym, 8, Features),
                            moreaction(Conj, Args),
                            (Conj = [],F.=Al;
                            Conj\-[], mergemods[[[action, A1]], Arge, Actions].
                            frame (F1, relation, Conj, Actions), F = {F1)}.
action(transcribe, Syn, F, Features) --> transcribeterm(Syn, F, Features),
```

```
moreaction(Conj.Args),
                            (Conj = [],F =Al;
                            Conj\={}, Margemods({{action,A1}},Args,Actions},
                            frame (F1, relation, Conj. Actions), P = [F1]).
action (promote, 6ym, F, Features)
                                     --> promoteterm(Syn, F. Features),
                            moreaction(Conj, Args),
                            {Conj = () P =Al:
                            Conj = [], mergemode (([action, A1]], Args, Actions),
                            frame(F1, relation, Conj. Actions), F = [F1]}.
action (generate, Syn, F. Features)
                                    --> generateterm[Syn,F,Features],
                            moreaction (Conj.Args),
                            {Conj = [].F =A1;
                            Conj\=[], mergemods([[action,Al]],Args,Actions),
                            frame (F1, relation, Conj, Actions), F - [F1] }.
action(cause, Syn, F, Features)
                                   --> Causeterm(Syn, P. Features).
                            moreaction (Conj. Args),
                            \{Conj = (), F - A1;
                            Conj\=[], mergemods(([action.Ai]], Args, Actions),
                            frame (F1, relation, Conj, Actions), F = [F1]).
% binds, phosphorylates and activates
moreaction(Conj,Args) --> sem_conjrest(Conjl),
                            oneaction (9em, Syn, A, Peatures),
                            moreaction(Conj2, Alist),
                           [Conj2 = [], Alist=[],Conj=Conj1, Args = [[action,A]];
                            Conj2 = [], Conj = Conj2,
                            addmod([action, A), Alist, Args) }.
moreaction((),(),$,$).
passiveconnect (Sem, [ven] . Target . Features) -->
                  sem beterm(),
                  connectact (Sem, [ven], Target, Peatures).
processpatt(A) --> disease(A).
processpatt (A) --> process (A) .
optbyorprepagent(first,A) --> byagent(A).
opthyorprepagent(second, A) --> prepagent(A).
opthyorprepagent(first,A) --> [], {A = x].
byorprepagent (first, A) --> byagent (A).
byorprepagent (second, A) --> prepagent (A) .
optbyagent(A) --> byagent(A).
optbyzgent(A) --> [], \{A = [x]\}.
byagent(A) --> [by],
               substances(A).
byagent(A) --> [by],
                nounactionpatt(A).
prepagent(A) --> withobject(A).
prepagent(A) --> toobject(A).
% prepagent(A) --> andobject(A).
prepagent(A) --> ofobject(A).
```

```
% optprepagent(A) --> byagent(A).
optprepagent (A) --> ofobject (A) .
optprepagent(A) --> withobject(A).
optprepagent(A) --> toobject(A)
optprepagent(Al --> andobject(A).
optprepagent(AI --> (), {A= (x)}.
ofobject(A) --> (of),
                nounactionpatt(A).
ofobject(A) --> [of],
                substances (A) .
ofobject(A) --> [of],
                actionof(A).
otobjecti(A) --> [of], substance(A). % to parse Binding of Fyn and Bad.
optofobject(A) --> ofobject(A).
optofobject([x]) --> ().
processobject(A) --> process(A). & can be expanded to nounactpatt, etc.
% optwithobject(A) --> withobject(A).
* optwithobject(A) --> [), {A = [x]}.
withobject (A) --> [with], substances (A).
toobject(A) --> [to], substances(A).
andobject(A) --> [and], substances(A).
prepobject (A) --> [to], substances (A).
prepchject(A) --> (with), substances(A).
optbyarg(A) --> [by],
actionarg(A).
optbyarg(A) --> substances(A).
optbyarg(A) --> [], {A = ['substance unknown']}.
prepopt --> [to].
prepopt --> [with].
prepapt --> [by].
prepapt --> [of].
prepopt --> [].
* toopt
toopt --> [to].
toopt --> {}.
% withopt
withopt --> [with].
withopt --> [].
            ~~» ['-'].
optdash
            -->[].
optdash
optof
             --> [ofl.
optof
              --> [ ].
/* optactionarg(A) --> actionarg(A).
optactionarg([]) --> (). */
optactionary(A) -->
      actionarg(A).
```

```
y there is no further argument
optactionsrg(A) -->
    \mathbf{D}_{i}
    \{A - \{1\}\}.
t substances(F) --> substance(F).
t substances(F) --> substance(F1),
              moresubstances (Conj. Plist).
               ( Conj = {], Plist = [), F = P1;
               Conj \= [].
k .
ŧ
              mergemods (P1, Plist, Args).
                  frame (F, relation, Conj, Args)
$ substances(F) --> substanceswithmods(F).
F substances(A) -->
                   proteins (A).
t subswithmods.txt
$ substances is saved in a symbol table (st);
t check for success/failure lat
Case where substances is in at and has been successful
substances(Pmt) --> checkst(substances,_,s.Fmt).
t Case where substance is in st as a failure.
substances(_) --> checkst(substances,_,f,_), {!, fail).
aubstances(F) -->
        encop ($0,$0),
      { \+ checkst {aubstances, 1, 8, _, 60, _) },
        1mode(Lmods). % left modifiers
        (several substances ([relation, Conj, First [Rest]), % conjoined substances
        rmode(Rmode), & right modifiers
* create list of lists containing distributed mods. of substances
      [ distributesubs (Dist, (First | Rest), Lmcds, Rmods),
* check Lmods - "no" F1 or F2 should be changed to no F1 and no F2
        fixeconj [Lmods, [rel,Conj], [rel,C2]],
       teplice([Conj,Dist],F)
        frame (F, relation, C2, Dist) };
* substances and modifiers without conjunction
        substance (D1),
        rmods(Rmods),
        [D1 = {Type1, Substance1 | ModsD1],
        delete(ModsDi, [], ModsD2),
        append([Lmods, Rmods], WodsD2, Allmods1),
        delete(Allmodel, [], Allmode2),
        frame(F, Type1, Substance1, Alimode2))),
        snoop(S,S),
       {addst(substances, 1, s, F, SD, S)}.
/* substances(8) --> snoop(80,80),
                  {\+ checkst(substances, 3 .s, _, 50, _)},
                   complex(F),
                  {addst(substances, 3, e, F, SO, S)}.
t no more substances- save failure
substances(_) --> addst(substances,0,f,_), {!, fail).
```

```
severalsubstances(F) --> substance(P1),
                         moresubstances(Conj, Plist),
                       { Conj = { ], Plist = { ], F = Pl ;
                         conj \= [].
                         addmod(Pl, Plist, Argal,
                         frame (F, relation, Conj. Args)
                       }.
% ' X, Y, and 2'
 moresubstances(Conj,Args) --> sem_conjrest(Conj1),
                           substance (P1),
                           moresubstances (Conj2, Plist),
                         { Conj2 = [], Plist = [], Conj = Conj1, Args = [P1];
                           conj2 \= [] .conj2\= /, Conj = Conj2.
                           addmod(Pl,Plist,Arge)
* to allow for substances with modifiers
moresubstances(Conjl, Args) --> sem_conjrest(Conjl),
                                substances (Args) , { i } .
more substances ([], []] --> (). % no conjunction
* distributesubs
* distributes left mode and right mode over list of findings creating
t list of lists of findings with mode
distributesubs([),[],_,_] :- 1.
distributesubs (Dist, [D1 [Tail], Lmods, Rmods) :-
        distributesubs (Dist2, Tail, Lands, Rands), & distributed for remainder
        D1 = [Type1, Substance1 [ModsD1],
        append ([Lmods, Rmods), ModsD1, Allmods1),
        delete(Allmods),[],Allmods2),
        frame (D, Typel, Substancel, Allmods2),
      . append([D], Dist2, Dist). & Combine findings to get list of findings
lmods(A) --> stateterm(F),
           {frame(A, state, F, '[])}.
lmods([]) --> sem_measure(_).
lmods[[]) --> [].
rmods([]) --> (].
stateterm(F) --> acclex(state, F).
* for past participle of createbond and breakbond actions, the target
$ is the word. ax.: phosphorylated, dephosphorylated, methylated
stateterm(F) -->
            snoop(SO,SO), & get the initial string
            createbondterm([ven), _._}.
            {SO = [6]_]}. *get the first word of the string
stateterm(F) -->
            snoop(90,80), % get the initial string
            breakbondterm([ven], _,_},
            (SO = [P[]]). Wget the first word of the string
* may have to add attachterm for 'bound'
```

```
† Taken from MedLRE grammar to handle '3 cm'
sem measure(M) -->
                   sem_premeasure.
                   stm_quantityterm(N);
                   optdash,
                   sem_measureterm(Unit),
                 { frame(M, measure, (N, Unit], []) }.
complex predicates added November 8, 1999
% CrkL-C3G complex
* ras: raf-1 association
% ras: raf-1 complexes
& shc-qrb2-sos
V TCR/CD3 complex
% p/CAP-p/CIP-CBP/p300-SRC-1 complex
Rae:Ref-1 complexes
complex(C) -->
                  proteins(P),
                  {P = [A,B]_I,A = {I,B,= {I}},
                   optcomplexword,
                 { frame(C, complex, [P}, []) }.
t a complex of NFAT4 with calcineurin
complex(C)
             -->
                   complexword,
                   complexarg(A),
                   {frame(C, complex, [A], [))}.
complexarg(A) --> [of], proteins(A).
complexarg(A) --> [between], proteins(A).
% a complex between MyD86, TRAK-2, and the IL-1Rs
complexarg(A) --> action(contain), proteins(A).
* Complexes containing BOB.1/OBF.1 and Oct proteins
proteins (P)
             --> protein(A),
                 moreproteins (P1),
                 {(A\=[]; append([A],P1.P})}.
moreproteins(A) --> proteinconnector,
                    proteins(A).
moreproteins([]) --> [].
proteinconnector ... ['-'].
proteinconnector --> ['/'].
proteinconnector --> [';'].
@ connector -->
                  (', '].
                             taken out not to conflict with relation in
f connector -->
                   (and).
                                                               moresubstances
probeinconnector(C) --> [with].
optconnector -->
                    proteinconnector.
optconnector -->
                    Π.
complexword --> {complex}.
complexword --> [complexes].
complexword --> ['signaling complexes'].
optcomplexword
                   --> complexword.
optcomplexword
                   ~-> [].
substance(A) --> protein(A).
```

```
substance(A) --> cell(A).
substance(A) -- species(A).
substance(A) --> structure(A).
substance(A) --> domain(A).
substance(A) --> gens(A).
substance(A) --> geneorprotein(A).
substance(A) --> aminoacid(A).
substance(A) --> smallmolecule(A).
substance(A) --> matter(A).
substance(A) - -> proteinsits(A).
                                         this will be modified later
substance(A) --> disease(A).
substance(A! --> complex(A).
protein(A) -->
    proteinterm(P),
    {frame(A, protein, P, ())}.
complex(A) -->
    complexterm(P).
    {frama(A, complex, P, [])).
cell(A| -->
    cellterm(P),
    {frame(A, cell, P, [])}.
species(A) ···>
    speciesterm(P),
    {frame(A.species,P.[]]}.
structure(A) -->
    structureterm(P),
    {frame(A, structure, P, [])}.
domain(A) -->
    domainterm(P),
    {frame {A; domain, P, () | }.
деле (А) -->
    geneterm(P),
    {frame(A,gene,P,[])}.
geneorgrotein(A) -->
    gpterm(P),
    -{ [x],
    \{(X = gene, frame(A, gene, P, []);
      X = protein, frame(A, protein, P, [1];
      X\= gene, X \= protein, frame(A, geneorprotein, P, [1])).
aminoacid(A) -->
    aminoacidterm(P),
    {frame(A, aminoacid, P, {))}.
smallmolecule(A) -->
    smallmoleculeterm(P),
    (frame(A, 'small molecule', P, ())).
```

matter(A) -->

```
matterterm(P),
    frame(A, substance, P, []) }.
proteinsite(A) -->
    proteinsiteterm(P),
    {frame(A, 'protein site', p, [])}.
discase(A) -->
    diseaseterm(P).
    {frame(A, disease, P, [])}.
process(A) -->
     processterm(Syn, F, Features),
     {frame(A, process, F,[)),!}.
process(A) -->
     processterm(P),
     [frame(A, process, P, {]}.!}.
% terminals
proteinterm(F)
                       --> acclex(protein,F).
complexterm(F)
                      --> acclex (complex, F) .
cellterm(F)
                      --> acclex(cell, F).
speciesterm(F)
                      --> acclex(species,P).
atructureterm(F)
                       --> acclex(structure, P).
domainterm(f)
                       --> acclex(domain, F).
geneterm(F)
                       --> acclex(gene,F).
gpterm(P)
                      --> acclex(gp, #}.
aminoacidterm(F)
                      --> acclex(aminoacid, F).
smallmoleculeterm(F) --> acclex(smallmolecule, F).
matterterm (F)
                      --> acclex(substance,?).
                      --> acclex(proteinsite,F).
proteinsiteterm(F)
diseaseterm(F)
                      --> acclex(disease,F).
processterm(F)
                       --> acclex(process, ?).
* action(activate, Syn, F, Features) --> activateterm(Syn, F, Features).
activateterm(Syn,F,Features) --> acclexes(activate, Syn,F,Features).
attachterm(Syn, F, Features)
                               --> acclexss(attach, Syn, P, Features).
breakbondterm(Syn, F, Features) --> acclexes(breakbond, Syn, F, Features).
createbondterm(Syn, F, Features) --> acclexes(createbond, Syn, F, Features).
inactivateterm(Syn, F. Features) --> acclexes (inactivate, Syn, F. Features).
                              --> acclexes (react, Syn, F, Peatures).
reactterm(Syn, F, Features)
releaseterm (Byn. F. Features)
                               --> acclesss (release, 6ym, F, Features).
signaltsrm(Syn, F, Features)
                              --> acclexss(signal, Syn, F, Features).
substituteterm(Sym,F,Features) --> acclexes(substitute, Sym,F,Features).
transcribeterm{Syn,F,Features} --> acclexes(transcribe, Syn,F,Features).
                              --> acclexss(promote, Syn, .Features).
promoteterm (Syn. F, Pastures)
                               --> acclexes (process, Sym, F, Features).
processterm(Syn, F, Features)
generateterm(Syn, F, Features) --> acclexes (generate, Syn, F, Features) .
causaterm(Sym, F, Features)
                               --> acclexes(cause, Syn, F, Features).
4 Semilist contains a phrase which is an action
actionchk(Semlist) :-
       intersect (Semlist, (attach, cause, createbond, breakbond, activate,
                  inactivate, substitute, transcribe, express, promote, signal)).
& Semlist contains a phrase which is a connector action
```



```
Genome sections: ends here
* relations are connected by conjunctions, or
k
           certain 'conn' prepositions.
t Taken from MedLEE grammar to handle connectives that are conjunctions
Ł
           Ex: "severe markings, possibly from tuberculosis"
sem_relation(F,[)) -->
                      % relation and modifiers
       жет_сотпаршис,
       sem certainty([],C,rel).
       prepterm (P. conn),
       \{frame(P,rel,P,C)\}.
       tplice([[rel,P],C],R).
           Ex: "markings, swelling", "markings and swelling"
sem_relation(R,[]) --> sem_conjrel(R),
                      вым фолтарипс.
          "density may represent known tumor"
    'markings, and swelling"
sem_conjrel(F) -->
      Bem commapune,
      sem_conjterm(Conj),
      {frame {F, rel, Conj, [] } }.
sem_conjrest(Conj) -->
                        * restricted conj, has not sem relation_showopt
       вет соннарилс,
       eem conjterm(Conj).
% "markings, swelling*
sem_conjrest(',') -->
     ancop(S0,S0),
       ает соппарилс,
     encop (8,6),
       {$0 \- S}.
* Treatment of Verbs from MedLER's Grammar
            form of "be"
sem auxvarb(B) --> sem beterm(B).
            form of "do"
sem_auxverb(B) --> sem_doterm(B).
            form of "have"
sem_auxverb(B) --> sem_baveterm(B).
sem_recrel --> prepterm(in, ).
sem_recrel --> prepterm(to,_).
t "is not"
sem_auxrel(V) --> sem_auxverb(_),
                sem_negterm(V).
sem_auxrel(V) --> sem_auxverb(V).
Left modifiers of findings include negation, quantity, certainty, degree, and
                                 change type modifiers
```

```
sem_integer(W) --> [W], {integer(W)}.
sem_integer(W) --> integerterm(W).
sem_timeunit(T) --> sem_timeunitterm(T).
t From MedLBE grammer . "lasting 2 days", "for 2 days", "times 2 days"
mem duration(F) -->
       sem durpreps,
        sem_premeasure, %about
        eem_timemeasure(T),
        sem_durationmod, t opt. - "in duration"
        {frame (P, duration, [T), [))}.
Bem_duration([],$,$).
sem_durpreps -->{times],
sem_durpreps -->
    prepterm(for, ).
sem_durpreps -->[lasting,for].
sem durpreps --> [lasting].
sem durpreps -->[lasted,for].
sem_durpreps -->[lasted].
sem durationmod -->
         sem_aposts, topt. - "'e"
        [duration].
sem_durationmod --> (in), [duration].
mem_durationmod --> [].
sem_aposts --> ['''], [s].
sem_apost --> [].
& sem_frequency taken From MedLEE's grammar
% "two times", "times two", "two times a/per week", "two times daily"
sem_frequency(F) -->
        Bem_freqterm(F1);
                             a _ouceπ
        sem_freqterm(F2),
                            t "a day"
        {frame(M, unitval, (F1, F2), []),
         frame(F, frequency, [M], []) ].
sem_frequency(F) -->
        sem_freqterm(M), % "gid", "daily"
        {frame(&, Erequency, M, []) ).
% "2 times".
sem_frequency[F} -->
        sem premeasurs,
        sem_quantityterm(M),
        sam_times,
      {frame (P, frequency, [M], ()}}.
* "times 2"
sem_frequency(Q) -->
        sem_times,
        sem_quantityterm(Q1);
        {frame {Q, frequency, Q1, []]}.
sem_frequency(F) -->
        [q], sem_quantityterm(Q),
             sem_timewrit(T),
        {frame [F, frequency, [unitval, [Q, T]], [])}.
```

```
sem frequency(F) --> sem_eachevery,
                      Bem_quantityterm(Q);
                      sem_timeunit(T);
                     (frame {F, frequency, [unitval, [Q, T, every]], []]).
#em_frequency(Q) -->
                        * "second"
        sem_ordinal(O),
        sem timeopt.
        [frame (Q, frequency, O, []) ].
sem frequency([],8,9).
sem_timeopt --> [time].
sem timeopt --> [].
sam_eachevery --> [each].
sem eachevery ... [every].
sem_times-->(times).
eem timea-->(x).
% Taken from MedLEE's grammar
negation modifier - "no" as in "no cardiomegaly"
sem negation(f) -->
        aam_negterm(N),
        {frame (F, neg, N, []) }.
* negation not present
sem_negation([],50,80).
t Taken from MedLEB's grammar
* quantity modifier - "two" as in "two masses"
sem_quantity(F) -->
       encop($0,90),
       { \+ checkst(scm_dates,1,s,_,80,_) }, % not a legitimate date
       sem_quantityterm(Q),
                                  * "2 or 3", "2 to 3"
       sem quantityrmod(_);
                                  % rule out '2 ma'
       ( \+ next wordunit (SO).
        frame (F, quantity, Q, [])
sem quantity([],SD,SO).
sem_commapunc([', '[S], 6).
sem commapunc(6,5).
                     -- acclex(conj.C).
sem_conjterm(C)
sem_dotsrm(D)
                     --> acclex(vdo,D).
sem_endmark([.]S],S).
sem_endmark([;|S],S).
sem_freqterm(F)
                     --> acclex(freq.f).
sem haveterm(H)
                     --> acclex(vhave, H).
integerterm(I)
                     --> acclex(integer, I(.
sem measureterm(M)
                    --> acclex(unit, M).
sem_medterm(M)
                     --> acclex (med, M).
sem_negterm(N)
                     --> acclex (neg, N) .
prepterm (P.C)
                     --> acclex(p, [P.C)).
sem_timeunitterm(T) --> acclex(timeunit,T).
```

```
* lexog - adapted from MedLEE lexicon
*********************** CLOSED WORD CATEGORY LEXICON $8894898946884888848888
*$$$4$$$$$$$$$$$$$$$
                         NEGATIONS
                                    *************
:-unknown(_,fail).
:-multifile(wdef/3).
wdef (cannot.neg. no).
wdef (neither, neg. no).
wast (never, neg, no) .
wdef (no, neg, no) .
wdef (non, neg, no).
voef (none, neg, no).
wdef (not, neg, no).
wdef (nothing, neg, no).
8888899989988888888
                         wdef('&',conf.and).
wdef('/',comj,or).
wdef('-',grammar,'-'}.
wdef('+',conj,and).
wdef(although,conj,and).
wdef (and, conj, and).
wdef (as.conj.and).
wdef (because, conj. and).
wdef(but,conj,and).
wdef(',',conj,',').
wdef (except, conj, no).
*wdef(if,grammar, if).
wdef {minua, conj, no}.
wdef (nor, conj, no).
wdsf{or,conj,or}.
wdef(that,grammar,that).
wdef (though, conj.and).
wdef (thru, conj, and).
woet (verses, conj.or).
wdef(versus,conj.or),
wdef(vs,conj,or),
wdcf (when, grammar, when).
wdef(where, grammar, where).
wdef (whereas, conj, and).
wdef (which, grammar, which).
wdef(while,conj,and).
wdef (who, grammar, who).
wdef(yet,conj,and).
፞፞፞ቕቔ፞፞፞፞ዼጜቔቔቔቔቔቔቔቔቔቔቔቔቔቔ፟፟፟፟፟፟፟ቝቔቝPOSITIONS ቔቔቔዼጜጜጜጜጜጜቔቔቔቔቔቔቔቔጜጜጜጜጜቔቔቔቔቔ
wdef (above, ploc, above) .
wdef(about,p,[approximately,nconn)).
wdef(about,ploc,about).
wdef (across, ploc, across).
wdef {abutting,ploc,near).
wdef (accompanies, p, (with, conn)).
wdef (accompanying,p, [with,conn]).
wdef(adjacent,ploc,adjacent).
wdef(adjacent, region, adjacent).
wdef(after.p,[after.conn]).
wdef(after,tprep,after).
wdef(along,p,[on,ncom)).
wdef(approximately,p,[approximately,sconn]).
wdef(around,p,[approximately,nconn]).
```

```
wdef(at,p,[at,nconn]). .
   wdaf(atop,p,[on,nconn]).
   wdef(before.ploc.before).
   wdef (before, tprep, before) .
   wdef (behind, ploc, behind).
   wdef (below, ploc, below) .
   wdef(between,plog,between).
   wdef (beyond, ploc. beyond) .
wdef(by,ploc, near).
   wdef (despite, p. [with, conn]).
   wdef (during, p. [during, conn] | .
   wdef (during, tprep, during).
   wdef (encasing, ploc, encasing).
   wdef (extending, p, (in, nconn)).
   wdefifollowing.p, [after,conn]).
   wdef (following, tprep, after).
   wdef (for,p, [for, ncoun]).
   wdef(from,p,[from,conn)).
   wdef(in,p,[in,nconn]).
   wdef (including, p, [with, comm]).
   wdef (into, p. (in, nconn)).
   wdef(involving,p.[of,nconn]).
   wdef (next, tprep, next).
   wdef(occupying,p,(in,aconn)).
   wdef (on,p, [on,nconn] } .
   wdef(of,p,[of,nconn]).
   wdef(over,ploc,oyer).
   wdaf (overlie, ploc, over).
   wdef(overlied,ploc,over).
   wdef (overlies, ploc, over) .
   wdef(overlying,ploc,over).
   wdef (prior, tprep, before) .
   wdef (near, ploc, near).
   wdef (radiating, ploc, radiating).
   wdef (regarding, p, [about, nconn]).
                                                                                        t 'Youghly 6 mm'
   wdef (roughly, grammar, roughly).
   wdef (since,p, [since,conn]).
   wdef [since, status, subsequent] .
   wdef (through, p, [in, nconn] ).
   wdef (throughout, p, [in, nconn] ).
   wdef(to,p,(to,nconn)).
   wdef(toward,p.[to,nconn]).
   wdef(towards,p,[during,conn]).
   wdef (under, ploc, below) .
   wasf (undermeath, ploc, below) .
   wdef(until,tprep,until).
   wdef (up, grammar, up).
   wdef(upon,p,[on,nconn]).
   wdef(via,p,[with,comn]).
   wdef(with,p,[with,conn]).
   wdef (within, p, [in, conn]).
   wdef (without, p, [no, conn]).
   *wdef(without, neg, no) .
   * PROFESTORY FOR THE PROFESTOR OF MEASURE OF THE STREET FOR THE PROFESTORY OF THE PR
   wdef{'%', unit, percent}.
```

```
wdef (cc, unit, cc).
wdef (centimeter, unit, cm).
wdef (centimeters, unit, cm).
wdef(cm, unit, cm).
wdef(degrees, unit, degree).
wdef (gm, unit, gram).
wdef (qms, unit, gram).
wdef (gram, unit, gram).
wdef(grame, unit, gram).
wdef (kg, unit, kilogram).
wdef (kilo, unit, kilogram).
wdef{kilogram, unit, kilogram}.
wdef (kilograms, unit, kilograms).
wdef (liter, unit, liter).
wdef (liters, unit, liter) .
wdef (microgram, unit, microgram) .
wdef (micrograms, unit, microgram) .
wdef(milliliter,unit,ml).
wdef(milliliters, unit, ml).
wdef(milligram, unit, mg).
wdef(milligrams, unit, mg).
wdef(milliseconds,unit,millisecond).
wdef(millivolts,unit,millivolt).
wdef(ml,unit,ml).
wdef(millimetar,unit,mm).
wdef(millimeters, unit, mm).
wdef(mm, unit, mm).
wdef (oze, unit, ounce).
wdef(percent, unit, percent).
ትርፍናትርፍትርፍት እንደ እና እርጀትር እና የመጠር ነው። የተለከተው የተለከተ የ
wdef(half,integer,'one half').
wdef(semi, quantity, semi).
wdef (ii, integer, 2).
wdef(iii,integer,3).
wdef (vi, integer, 4).
wdef (v, integer, 5).
wdeflvi.integer.5).
wdef(vii,integer,7).
wdef(viii, integer, 0).
wdef(ix, integer, 9).
wdof(xii,integer,12).
wdef(xiii,integer,13).
wdef(one,integer,1).
wdef(two,integer, 2).
wdef(double, quanticy, double).
wdef(three,integer,3).
wdef(four,integer,4).
wdef (quadruple, guantity, quadruple).
wdef (five, integer, 5).
wdef(six,integer, 5).
wdef(sixty,integer,60).
wdsf(seven,integer,7).
wdef{eight,integer,8}.
wdef (nine, integer, 9) .
wdef (ten, integer, 10).
wdef {eleven, integer, 11}.
wdef {twalve,integer,12}.
```

```
wdef (thirteen, integer, 13) .
 wdef (fourteen, integer, 14) .
 wdef (fifteen.integer, 15).
 wdef(sixteen.integer,16).
 wdef (seventeen, integer, 17).
 wdef (eighteen, integer, 18).
 wdef (nineteen, integer, 19).
 wdef(twenty,integer,20),
 wdef (thirty, integer, 30).
 wdef (forty, integer, 40).
 wdef(fifty,integer, 50).
 wdef(sixty,integer,60).
 wdef (seventy, integer, 70).
 wdef (eighty, integer, 80).
 wdef (ninety, integer, 90).
 wdef (hundred, integer, 100).
 wdef(thousand,integer,1000).
 wdef (million.integer, 1000000).
 wdef (billion, integer, billion).
 wdef (zero, integer, 0).
 wdof (first, ointeger, 1).
 wdef (second, pinteger, 2).
 wdef(third,ointeger,3).
 wdef (fourth, ointeger, 4) -
 wdef (fifth, cinteger, 5).
 wdef(sixth,ointeger,6).
 wdef(seventh.ointsqur.7).
 wdef(gighth, ointeger, 8).
 wdef(ninth,ointeger,9).
wdef(tenth, ointeger, 10).
 wdef(eleventh, pinteger, 11).
 wdef(twelvth,ointeger,12).

    wdef(thirteenth,ointeger,13).

 wdef (fourteenth, ointeger, 14).
 wdef(fifteenth,ointeger, 15).
 wdef(sixteenth,ointeger,16).
 wdef (seventeenth, ointeger, 17) .
 wdef (eighteenth, pinteger, 18).
 wdef (ninttenth, ointeger, 19).
 wdef(triple, quantity, triple).
 wdef (twentisth, ointeger, 20).
 wdef (thirtieth, ointeger, 30).
 wief (single, quantity, 1).
 wdef (colitary, quantity, 1).
 wdef (frequency, grammar, frequency) .*/
 wdef ( ', grankhar, '.').
.wdef(';',grammar,')').
 wdef('/',grammar,'/').
 wdef(':'.grammar,':').
 wdef('?', certainty, 'moderate certainty').
 wdef('+',certainty,'high certainty').
 wdef{'''', grammar, ''''}.
 wdef (once, freq. 1).
 wdef(times, grammar, x).
```

wdef(twice, freq. 2).

```
* lexicon with lexig containing common English words adapted from lexi of
 MedLEET
 * lexis from lext of MedLEE
 * August 23, 1999
 . CAROL FRIEDMAN
           QUEENS COLLEGE, COLUMBIA UNIVERSITY
                                                                        ٩
                     · Version 3.0 4-01-00
                       Version 2.0 1-31-96
                       Version 1.0 1-5-92
                       SEMANTIC LEXICON FOR CLINICAL TEXT
 ŧ
    The lexicon consists of several files:
       lex0g.pl: single word closed classes
       lexig.pl: single word - general modifier type words:
      wdef (category, target).
          word - is the name of the word being categorized;
 1
           category - is the semantic category for the word
           target - is the canonical/standard form for the word
 ¥
                      words which are synonyms should be assigned the same
 ķ
                      canonical form.
                                                                         ŧ
 ŧ
      multi-word phrases are categorized as follows:
                                                                         ŧ
       phrase (word, category, phrase, target).
 ŧ
                                                                         ŧ
     Semantic Catagorics:
 k
         certainty "possible"
                canonical values limited to: moderate - for possible
                                            high - for high possible
                                            low - for low possible
 ŧ
         conj - relational operators "and", "or", which connect one finding &
 Ł
 ٠
                to another finding
        neg - negation "no", "not"
         quant - for quantitative information "many"
 :-unknown(_,fail).
:-ensure loaded([nsphrase,lex0g,lex1g,lexsemact,lexsyn,lexsub]).
```

*/

```
द definitions kept from MedLER lexicon - lex1.pl
wdef (be, vbe, 'high certainty').
wdof (been, vbe, 'high certainty') . .
wdof(being, vbe, 'high certainty').
wdef(was, vbe, 'high certainty').
wdef(is, vbc, 'high certainty').
wdef (were, vbe, 'high certainty').
wdef (became, voertainty, 'high certainty').
wdef (become, vcertainty, 'high certainty').
wdef (becomes, vcertainty, 'high certainty').
wdef (becoming, vcertainty, 'high certainty').
                              put in action lexicon
wdef (changed, change, change).
wdef (changes, change , change) .
wdef (changing, change, change).
wdef (necessarily, cortainty, 'high cortainty').
wdef (necessary, vrecommend, recommended).
wdef (necessitate, vatatus, need) .
wdef (necessitated, vetatus, need).
wdef (necessitating, vstatus, need).
wdef (necessitates, vstatus, need).
wdef (need, vetatus, need) .
wdef (needed, vstatus, need).
wdef (needing, vstatus, need) .
wdef (needs, vstatus, need).
```

28

```
file ml_parger.pl
:- multifile(phrase/5).
; - multifile (wdef/3).
:-unknown(_,fail).
t Load in program components - library components are part of Prolog
:- ensure_loaded([library(basics], library(not), library(lists).
   library (readin), library (etringe), library (ctypes), library (readconst),
   library(date), library(listparts), library(sets),
   radrec, radpardb, useful, util, tagging, lexicon, gengram] }.
t:- initialization run.
trun :- on_exception(Error, processrun, stop(Error) ].
runtime_entry(start) :- processrun.
runtime_entry(abovt) :- halt.
* process report
processrum :- process, halt.
tstop(Error) :-
    write (user error, 'Error: '), write (user_error, Error), halt.
* get user supplied parameters and process report
procesa :-
get_args(Mode, Infile, Outfile, Pro, Undefs, Protocol), 1,
            (Examtype = []; * must have a domain
            process(Infile, Dutfile, Prb, Undefs)).
* open Infile (text input) and process
process(Infils, Outfile, Prb, Undefs) :-
           see (Infile), seen, see (Infile),
           on exception (Error,
           test_genome (Outfile, Prb, Undefe) .
                app_erro(_, Cutfile, Error)),
           closefiles (Dutfile, Prb, Undefs) .
process(_,Outfile,_,_) :-
        app_err(_,Outfile,'Program failed').
app_err0(_,Output,Error) :-
       tell (Output),
       write('<error>'),
       write('Prolog Error occurred: '),
       app_err(_,Output,Error).
app_errl(_,Output,Error) :-
       tell(Output),
       write ('cerror>').
       write('Error in input: '),
       app_err(_,Output,Error).
app_err(_, Output, Error) :-
       tell(Output),
       write(Brror), write('</error>'), nl.
closefiles (Outfile, Errfile, Unfile) :-
      tell (Outfile), told,
      (Errfile = []; tsll(Errfile), told),
      (Unfile = []; tell(Unfile), told[.
```

```
Argument options - get user defined arguments
% -p ProbPile (Otherwise default is problem messages are not written to file)
* -i Infile (if input is supplied by file and not standard input
* -s Section (default is impression)
* -m Mode (default is relax; the three choices are strict, relax, skip)
4 -o Outfile (if output should be file and not standard output)
* -? Provide list of default arguments
* -u Undefs (otherwise default is - undefined messages are not written
      to a file}
get_args(Mode.Infile,Outfile,Prbfile,Undefs,Protocol) :-
    unix (args (Args)),
  (Args = [], |, writesyntax;
   Args = ['?'],!, writesyntax;
   Arge - [X Rest], I,
   set_args([X|Rest), Mode, Infile, Outfile, Prbfile, Undefs, Protocol||.
writesyntax :-
     write (user_error, 'genepareer [-m Mode] '),
     nl (user_error),
     write (user_error, '
                                 [-t Outtype] [-p Probfile] [-u Undefs]'],
     nl (user_error) ,
     write(user_error, '
                                [-i Infile] [-o Outfile] '),
     nl (user_error) .
```

% nsphrase.pl - contains words/phrases that are ignored nosem(both,[both]). nosem(however,[however]). nosem(selectively,[selectively]). nosem(specifically,[specifically]). nosem(the,[the]).

```
% file radpardb.pl
ֆ յուռe 25, 1999
a fail an unknown predicate
 :-unknown(_,fail).
:- op(900, fy, [not.once]). * same priority and type as \+
:- op(700, xfx, [\=,-=]). * s me priority and type as = or ==
:- dynamic(sentno/1).
% \sem\radpardb.pl
tparse_sentences(*Beg,-Fmt,-ParseErrors,-Undefineds,-Unsents,*6cction,
                 +DzerMode, +Examtype, Sentno, Outsno, Inc$no)
        Beg is list of sentences, Pmt is list of target forms,
        ParseErrors are a list of sentences which could not parse,
$
8
        Undefineds is a list of undefined words in sentence
        Unsents is a list of sentence containing undefined words
        Section is the section of the examination. UserMode is the
        parsing mode specified by user,
        Examtype is the domain (type of exam)
        Sentno is the number of the starting sentence
        Outsno is the last sentence number + 1
ar.
        IncSno is the amount that the sentence number should be increased
4
             (i.e. it is 1 when called by paree sects and 0 when in
               recovery mode)
    Each sentence is parsed independently.
parse_sentences([],(],(],(],(),[],_,_,_,_) :- !. %no more sentences
parse_sentences(Beg,Fmtlist,Outfail,Outundefs,OutunSents,
                 Section, UserMode, Examtype, _, _, IncSno) :-
    got sentence (Beq.S.Rest), !,
    ( isidentifier(8), !, % ignore identifier sentences - parse remainder
      parse_sentences {Rest, Fmt1, Outfail, Outunders, OutunSents,
                 Section, UserMode, Examtype, ___, IncSno), |,
       (outputform(htext), S \= ['.'], !, IncSno \= 0, *D means in recovery
mode
        append([[[sentence,S]]],Fmtl,Fmtlistl;
        Fmtlist = Fmtl
      % ( Incano = 0, ); % on same sentence in recovery mode
      * sentro(Sno), NewSentro is Sno + IncSno,
      * retract(sentno(_}), assert(sentno(NewSentno))
    f Inceno = 1, write('***'), write_list($,3,_}, nl, |,
    % Incano = 0,
      preprocess(S,Bs,Undef,Semlist,strict), t bracket and check for undefineds
      parse modes (S.Bs. Scmlist, Pmtl, Errors, Undef, Unsents, Section, Writefail,
                  Examtype, UserMode, IncSno), & parac first sentence
      parse sentences (Rest. Fmt2. Moreerrors, Moreundefs, MoreUnSents,
                  append (Errors, Moreerrors, Cutfail),
                                             * Combine failures
      (outputform(htext),
            (Fmt1 = [], IncSno = 0,
             Fmt2 = [], Fmtlist = Fmtl , !
```

```
append (Fmt1, Fmt2, Fmtlist)
                    % Combine targets
      append (Unsents, MoreUnSents, OutunSents), & Combine sentences
      append (Undef, Moraundefs, Outundefs)
                                               % Combine undefined words
*parse_modes(+6,+8s,+Semlist,-Fmt,-Failures,+Undef,-Unsents,+Section,
     +WriteMessage, +Examtype, +Mode, +IncSho)
        S is original sentence; Re is sentence after lexical lookup
*
        Semlist is list of semantic categories in sentence
ŧ
        Fmt is formatted output,
ŧ
        Failures is list of sentences/fragments which could not be parsed.
ŧ
        Undef are words not in lexicon, Unsents are sentences containing
f.
                undefined words
8
        Section is name of section being processed
Ł
        WriteMessage is message returned from doresult (in case doresult fails)
8:
        Exampype is domain, Mode is user specified mode
        Income is 0 if this is a fragment of a sentence that was already
ŧ
                parsed - but unsuccessfully; is 1 if this is a new sentence
* Best possible - try to get the most accurate parse possible trying
% all alternative strategies in turn if neccessary
* All words in sentence are defined
parse modes (S. Br. Semlist, Fmt, Errors, [], [], Section, no, Examtype, Pmode,
              Inc) :-
       (Pmode = bpseg, Pmodemod = mode2, !; %in recovery mode
       Prode = bpseg2, Prodemod = mode2, 1;
       Pmode - bpsegl, Pmodemod - model, 1;
       Prode - Dpskip, Prodemod = mode4, !; %in recovery mode % in user specified parse mode - don't parse in mode 5 or keyword
       Prode \- keyword, Prode \- modes.
       Pmodemod = model
       ).
      dosent(9,Bs,Semlist,Fmt1,Message,Section,_,Examtype,Pmodemod,_),!, }
strict first
      recovery(_,9,8s,Semlist,Fmt2,Message,Errors,[],[],Section,
                  Pmode, Examtype, _), * try alternative modes if neccy
       (outputform(btext), inc \= 0, 1, append([[[sentence,S]],Fmt1,Pmt2],Fmt);
       append (Fmt1, Fmt2, Fmt)
& alternative strategies if have undefined words
parse_modes(8,8s,Sem)ist,Fmt,Errors,Undef,Unsents,Section,no,Examtype.
             Pmode, Inc) :-
     Undef \= [],
     recovery(_,S,Bs,Semlist,Fmtl,yes,Errors,Undef,Unsents,Section,
                 Pmode, Examtype._), % try alternatives if have undefineds
      {outputform(htext), Inc = 0, !, append!([sentence,3]],Fmt1,Pmt);
     ١.
% key word strategy is fastest but least reliable;
parse modes (3, Bs, Gemlist, Fmt, Errors, Vodef, Unsents, Section, no, Examtype,
             Pmode, Inc) :-
     [Pmode = keyword: Pmode = mode5
     ; Pmode - mode5},
     recovery (5, S, S, Semlist, Fmtl, yes, Errors, Undef, Unsants. Section, Pmode,
               Examtype,_),
      (outputform(htext), Inc \= 0, (, append([[sentence.5]],Fmt1,Fmt);
```

```
Fmt1 - Pmt
     ١.
† Parsing/Recovery modes
t parse_modes(+Ltvel,+s,+Bs,+Sem,-Fmt,+Failed,+Undef,+Unsents,+Section,
              +Pmode, +Examtype,_)
    Level is the recovery level of the predicate
    S is the original sentence list
ŧ
    Bs is the
Ł
    Sem is the list of semantic categories in the sentence
    Fmt is the formatted output for the sentence
    Failed is 'yes' if the parse was unsuccessful, and 'no' otherwise
    Undef is a list of words in sentence which are undefined (not in lexicon)
    Unsents are the lists of sentences/segments which could not be parsed.
    Section is the section of the report
Pmode is the user specified parse mode
8 Examtype is the domain
% mode 1 is the atrictest parsing mode - the parser succeeded for the complete
         original sentence using the grammar; all words in original sentence
ŧ
         are defined in lexicon
% mode 1 - alternative not needed because parse succeeded
recovery(1,_,_,,[],no,[],Undef,Unsents,_,_,_,) :- |.
         - no alternative strategy allowed in mode 1
            in case where there are no undefineds, Noparse is S
recovery(1,$,_,_,[],yes,8,[],[],_,Pmode,_,_) :-
         Pmode = strict; Pmode = model, |.
            in case there are undefineds, Unsents is S
recovery(1,8,_,_,[],yes,Noparse,Undef,Unsents,_,Pmode,_,_l :-
        (Pmode = strict; Pmode - 'mode1'),
        Undef \= [], Ungents - S, Noparse - [], 1.
recovery(1,8,_,Semlist,[],yes,S,_,_,_,_,_,_, :-
* sentence contains no relay, information, don't try to recover
      \+ (subtype(finding,Semlist); subtype(time,Semlist)), |...
\+ actionchk(6emlist). % april 23, restored
% mode 4 - skip undefined words and try to parse according to mode 1
recovery (4.5., Fmt, yes, Errors, Undef, [], Sect, Pmode, Examtype, _) := Undef \mathbb{T} [],
         (Pmode = bp; Pmode = mode4;
          Fmode = bpseg; Pmode = bpskip; Pmode = mode4
         ١.
         preprocess(8, Bs,_,Semlist, bpskip),
         dosent(S, Bs, Semlist, fmt1, Message, Sect, _, Bxamtype, mode4, _), |,
         recovery{_,Bs,Bs,Samlist,Fmt2,Message,Errors,[],[],Sect,
                      bpskip, Examtype, Sentnol. & try alternatives if neccy
           append(Fmt1,Fmt2,Fmt).
t mode 3 - try longest parsed segment; partition rest of
             sentence using mode 5 for paras mode hp
recovery [3,8,88,_, Fmt, yes, Errors, Undef, Unsents, Sect, Pmode, Examtype,_) :-
         % allowable modes for choosing longest segment
         (Pmode = bp; Pmode = bpakip;
          Prode = skip; Prode = mode3; Prode = mode4;
          Pmode = bpseg3; Pmode = bpseg
         (Pmode = bpskip, Pmodemod = mode4 3;

    Prodemod = mode3

         checkst(sem pattern, .s.Target, Bs.Rest), tcheck symbol table
```

```
tdooreault(Target, Pmt1, Examtype, Sect, Pmodemod, _);
           formatresult (Target, Pmodemod, Pmt1).
          {Pmode = mode3, Fmtlist = (], Errors = Rest;
          recovery(5, Rest, Rest, Fmtlist, yes, Errors, Undef, Unsents, Sect,
                         Pmode, Examtype, ]
          append (Fmt1, Pmtlist, Pmt).
? mode 2 segments sentence using word barrier methods. This mode is tried if
           parse failed for original sentence/or there are undefined words
*
             segment sentence using word berriers
recovery(2,5,_,_,Fmt,yes,Brrors,Undef,Unsents,Sect,Pmpde,Examtype,_) :-
          (Pmode = bp: Pmode = bpskip; Pmode = mode2; Pmode = skip;
          Prode = mode2; Prode = mode3; Prode = mode4;
           Pmode = bpseg; Pmode - bpseg2;
           Pmode - bpseg3
          segmentandparse(S, Fmt, Errors, Unsents, Sect, Pmode, Examtype, _), !.
* mode 5 - try to partition sentences by findings
* when a finding in sentence is found, go left until first
    modifier is found (if 2 Eindings are next to each other, 2nd one
    is considered the finding and lat is considered the modifier)
    Repeat searching for successive findings using this method
recovery {5, [], [], _, [], _, [], _, _, _, _, _, _, ... ;- (.
recovery (5, 5, Bs, _, Pmt, yes, Errors, Undef, Unsents, Sect,
                Paode, Exambype, _) :-
          (Pmode = bp; Pmode = bpskip; Pmode = bpseg; Pmode = keymode;
          Pmode - mode5; Pmode - negmode
         ١.
          preprocess(8,Bs1,_,_,bpskip), % skip undefined words
          actionfindingseg(Bal, Pseg, Before), 1, % get segment containing finding
           (Feeg = [], Errors - S, 1; % no finding to segment
           *Before > (), Errore = Bs, Fmtl * [], 1; t this part was tried
           preprocess (Fasg, Basg, _, Semlist, bpskip), dosent(Fasg, Basg, Semlist, Fmtl, Message, Sect, _, Examtype,
                    modeS,_! * try to parse finding segment
            (Before = [], Before1 = [], Message = yes, !; % no segmenting yet -
skip beg.
            Massage = yes, Beforel = Before, !; *don't add '.'; have to skip
more
            append (Hefore, ['.'], Beforel)
            [ Faeg = [], Fmt . [], !; % no finding left in sent. - don't recover
           recoverrest (Fseg,__, Beforel, Fmt2, Message, Errors,
                      Sect, Newmode, Examtype, ),
            * recover remainder
            append (Fmt1, Fmt2, Fmt)
* nothing could be recovered; all input -> Errors ; Format is []
recovery(_,Sente,_,_,[],yee,Sents,Undef,[],_,_,_,).
 part of phrase was skipped. add period and treated skipped part as a
1 sentence
t recoverrest(+Segment,+Semlist,+Before,-Fmt,+Message,-Failures,+Section,
        +Mode,+Examtype,_}
        Segment is part of sentence with a finding
```

```
Semlist is a list of semantic categories for that sentence part
٠
        Before is the part of sentence before Segment
        Fmt is the format for this segment
٩
        Message is 'no' if there is no segmentle information to be recovered
4
                Message is 'yes' otherwise
۲
        Pailures are lists of segment(c) that could not be parsed successfully
¥
        fection is section being processed, Mode is user specified parsing mode
        Examtype is domain
recoverrest(__,_,Before,(),no,Before1,_,_,_) :-
  (Before = []. Before1 = [], 1; % nothing was skipped
   append(Before,['.'],Before1)
* nothing left to recover; write phrase that was skipped
recoverrest([],_,Before,[],yes,Before1,_,_,_, :-
   {Before - [], Before1 = [], !/
   append(Before,['.'),Beforel)
   ), !.
% can recover partial paree
recoverrest(B$,_,Before,Fmt,yes,Errors,Sect,Pmpde,Examtype,_) :-
         checkst(sam_pattern, _.s, Target, Bs, Restseg), % recover from symbol tab.
         tdoresult(Target, Fmtl, Examtype, Sect, mode5, ),
          formatreault (Target, mode5, Fmtl),
         recovery (5, Restseg, Rest, _, Fmt2, yes, Error2,
                    [],[],Sect,Pmode,Examtype,],
         append (Fmtl, Fmt2, Fmt),
                                               tnothing skipped to add '.' to
          (Before = [], Srrors = Error2, i;
          append(Before, ['.' [Error2], Errore)
* cannot recover partial parse - skip first element and retry
t if let element is a negation semantic type, skip 2nd element instead
      Handles case where 1st element is a negation, certainty or status
        add 2nd element to unparsed sentences list (enloosed in angle brackets).
recoverrest([X,Y|Restseg],_,Beforel,Fmt,yes,Errors,
                      Sect, Pmode, Examtype, _ > :-
         foundword (X, Seml, Tar),
          ( member(Sem1, [neg, certainty, vcertainty, vconn, status, vetatus));
           Sem1 = p, Tar = [\_,conn]
         ٠,
          % (Mod = neg; Mod = certainty; Mod = status; Mod = vcertainty), % leave
this mod in
          preprocess([X|Restseg] FsegO,_,_,bpskip), % skip undefined words
findingseg(FsegO,Fseg,Esfore21, !, % get finding seg
           {Pseg = [], Errors = [X,Y|Restseg], Fmt = []; * no finding
           preprocess(Feeg, Baeg, _, Restsem, bpskip), t skip undefined words
           dosent (Faeg, Saeg, Restsem, Fmtl, Message, Sect, _, Examtype,
           Sect, negmode, Examtype, _}, % recover remainder
            (Beforel - [], Errors = Error2, 1;
            append(Beforel, [. | Errors), Errors)
           ١.
           append(Fmt1,Fmt2,Fmt)
          ۶.
    skip 1st element; enclose it in brackets
recoverrest ([X | Restseg],_, Before1, Fmt, yes, Errors,
                 sect, Pmode, Examtype, ) :-
          preprocess (Restaug, PacgO, _, _, bpskip),
```

```
findingseg(Fseg0,Fseg,Refore2), 1, % get finding seg
          append(Beforel, [X|Refore2), Before).
          (Fseg - [], Errors = (X{Restseg], Fmt = {]; % no finding
           preprocess (Fseg, Bseg, _, Resteem, bpskip),
          dosent (Fseg, Bseg, Restsem, Fmtl, Message, Sect, _, Examtype,
                   mode5, ), & try to parse finding segment
          recoverrest (Pseg, _, Before, Pmt2, Message, Errors,
                     Sect, Newmode, Examtype, _), % recover remainder
          append (fmt1, Fmt2, Fmt)
* no semantic information left; return Errors
recoverrest ([X Restseg], []; Beforel, Fmt, yes, [X Restseg],
                Sect, Pmode, Examtype. . ) .
*dosent(+5,+Bs,+Semlist,-Fmtlist,+Message,+Section,+WriteMessage,+Examtype,
        +Mede)
       S is original list of words in sentence; Bs is list after lexical lookup
ŧ
       Semliat is list of semantic categories corresponding to Be
¥
Ŀ
       Emtlist is list of target forms for sentence
       Message is 'yes' if the output from parser signals a failure,
٠
                and 'no' otherwise
ŧ
       Section is section of examination being processed
       WriteMessage eignals whether an error occurred in generating target form
       Examtype is the domain, and Mode is the user specified mode of parsing
* Parse sentence and returns target in nested format
% Handles case where sentence should be skipped because info is about
    family member or peripheral to patient
dosent(S,_,Semlist,(),Error,_,_,_,_, :-
  skipsentence(S, Semlist, Error), 1.
dosent(S,Bs,Semlise,Fmtlist,Brrormeg,Section,Writefail,Bxamtype,Mode,_) :-
   attemptparse (P.Ss. sentence, Semlist, Section, Atotal),
   ( P = (failure), Errormsg = yes, Writefail = no, ! * parse failure
      P = [], Errormeg = no, Writefail = no, Pmtlist = [], ! % empty target
      formatreault (P, Mode, Fmtlist),
        Errormeg = no, Writefail = no, |
      Errormeg - yes, Writefail = yes, !
*parse_sentences(Beg, Beg, [], [], _, _, _) :- !.
% attemptparee(-P,+8s,+Structure,+Semlist,-Ptype,-Total)
        P is output from parser
        Be is list of words in sentence after lexical lookup
Ł
        Structure is name of structure to be parsed
        Semlist is list of semantic categories corresponding to elements in Be
        Total is number of times parser reached sem_sent in grammar;
                 where sem_sent is highest level predicate in grammar
t don't parse if sentence consists of only '.' or ';'
attemptparse([],Bs, , , , , ) :-
Bs = ['.']; Bs = [';').
& if a template exists for whole sentence, get parat from it
```

```
attemptparse(P,Bs,sentence,_,_,):-
Bs = \{X, \cdot, \cdot\}, is_light(X), $ the whole sentence is a finding
   find sem_sent(P,X), !.
t parses and retracts wellformed string table - parses sentence
attemptparee (P, Bs, sentence, Semlist, Ftyps, Atotal) :-
   retractall(wfst(_,_,,_,,_,)),
retractall(addstotal(_)),
   sem sent(P,Semlist,Atotal,Bs,[]). !.
t parses and retracts wellformed string table - parses bodypart only
attemptparse(P.Bs.bodypart,_,_,) :-
   sem bodyloc(P.Bs.()),
   retractall(wfst(_,_,_,_,_,_)}, !.
taggmentandparse ( - Sentences, - Fmtlist, - Pailures, - Unsent, + Section, + Mode,
        +Exambype,+Sentno)
        Sentences is list of sentence segments.
        Fmtlist consists of the formatted output for the segments
Ł
        Failures is the list of unparsed segments.
        Unsent is the list of segments with undefined words.
        Section is the section being processed, Mode is the user specified mode
        Examtype is the domain and Sentro is the sentence id.
segmentandparse([],[],[],[],[],_,_,] := 1.
segmentandparse(Sentences,Fmtlist,Failures,UnSent,Section,Mode,
                   Examtype, Sentno) :-
     get_sentence(Sentences,S,Rest), 1, %sentence to segment
     preprocess(S.Sl., Samlist, Mode), 1,
     (Mode - mode2, NewPmode - bpseg2, 1;
      Mode = mode3, NewPmode = bpseg3, !;
      NewPmode - bpseg
        segment1(91,5egs,[],seg), |,
         parse_sentences (Segs, Fmt1, Fails, _, Un1, Section, NewFmode, Sxamtype,
                             Santno, Sentno, 01, !
      ; aegment2($1,θeg$,[],seg}, ι,
         parse_sentences (Segs, Fmtl, Fails, _, Unl, Section, NewPmode, Examtype,
                             Santno, Sentno, C), |
      ; segment3 {$1,Segs, [},Negstatus,seg}, !,
         paras_santences(Gegs, Fmtl, Fails,_, Unl, Section, NewPmode, Examtype,
                             Sentno, Sentno, O), i
       taile if cannot segment sentence; otherwise segments remainder
      segmentandparse (Rest, Pmt2, Nexterrors, NextUns, Section, Mode,
                          Examtype, Sentno),
      append (Fmt1, Fmt2, Fmtlist),
      append (Un1, NextUns, UnSent),
      append (Fails, Nexterrors, Failures), I.
toegment1(+5,-Segs,+Beg,+Message)
        S is list of words in sentence
Ł
        Segs consists of sentence segments as separate sentences
        Beg is list of words in sentence prior to the current portion of sentence
$
        Message is 'seg' if segmenting succeeded and 'noseg' otherwise
segment1{[],[],_,noseg} :- 1.
* segment sentence at connect phrase/word or at most conjunctions
* if negation precedes, restore negation
```

```
segment1({X|Rest},['.','<cos>'|Rem],Beg,seg) :-
     \+ sem_endmark(Rest,[]), * don't asyment if at end already
     foundword(X,Sem,Target), & get semantic classification and target
     ( X = nor, append([no], Rest, Rem) % ok to segment at nor
      :X = without, append([no], Rest, Rem) t ox to segment at without
      %;X = 't', Rest = Rem
      ; Sem - neg. Rest - [Next|Rest2], t have negation; test word after
        foundword(Next.Sem2, Target2). & for connective - add back negation
         testforconn(Next, Sem2, Target2), Rem = [X|Rest2]
      ; testforconn(X, Sem, Target). Rest = Rem
     ١.
segment1((X{Rest], (X|Newrest], Start, Seg) :-
       append(Start, (X), Beg), % part before segmentation
       segment1 (Rest, Newrest, Seg, Seg) .
testforconn(X,Sem,Target) :-
      [ Sem = p, Target = [P,conn], P\= with * segment at connective prep
      ; member (Sem, [vecons, valow]) - % segment at these types of verbs
      // Sem = conj, \+ member(X, [and, or, ', ', '/', as))
      1.
% segment at certain words -
segment2([],[],[],noseg) :- 1.
segment2(S,Segs, [], seg) :-
        Beg2(S,Rest,Segs),
        \+ sem codmark(Rest,[]), !.
segment2([X Rest], [X Newrest], [], Seg) :-
       segment2 (Rest, Newrest, (), Seg) .
seg2([X]Rest],Rest,['.','<eos>'[Rem]} :-
        member (K, [which, that, until, where, when, while, who,
         '(',']', between, whereby, after, before, prior,
         greater, ranging]),
        Rem » Rest, !.
segment3([],[],_,_,noseg) :- !.
* segment at conjunction - if negation preceded conjunction, add
segment3((X|Rest),Rem,Beg,Megstatus,seg) :-
       \+ sem endmark(Rest,[]), !, % already at end of mentence
        Beg3([X(Rest], Rem, Beg, Negstatus, seg), |...
seg3([X|Rest],Rem,Beg,Negstatus,seg] :-
        wdef(x,conj,_),
        member(X,[and,or,',']),
        (nonvar(Negstatus), Rem = ['.', Negstatus Rest], | trestore negstion
         ; Rem = ['.','<eos>'[Rest], !
seg3([X]Rest],[X,'.','<eos>'[Rest], , ,seg) :-
       foundword(%,age), !.
segi{[X|Rest], (X|Newrest], Start, Negstatus, Segi :-
        ( nonver(Negatatus), ); } list meg already found - continue segmenting foundword(X, Sem, Target), !
            ( Target = no, Negstatue = X, !:
              Sem = neg, Negstatus = X, !/
              Sem \= neg, Target \= no, !
            ١,
```

```
* file radrec.pl
% September 7, 1999
fail an unknown predicate
:-unknown(_,fail).
                                  % same priority and type as \+
:- op (900, 'fy, (\+,not,once)).
;- dynamic(domain/1).
                                * domain being processed
                                % form of output (needed to distinguish
:- Gynamic (outputform/1).
                                t markup of text from formatting forms
; - dynamic(currentsect/1).
                                * section for outputting results
test genome (Outfile, Brrfile, Unfile) :-
    get_inputsents([], Toklist), !, % read in and tokenize input
                        $ error condition
     (Toklist = [], !,
      app_err1{_,Outfile,'No input sent'), !
     parse_sentences (Toklist, Fmtlist, Failed, Undef, UnSent, impression,
bp,genome,_,_,0),!,
     outputresults (Fmtlist, Failed, Errfile, Undef, Unfile, Unsent, Outfile,
                    full, line, genome, 1, 0, _, exe, plain)
     ١.
outputresults[FmtlistO,Failed,Errfile,Undof,Unfile,UnSent,Outfile,
                Amount, Type, Exam, Compno, DocComp, NewCompno, Caller, Protocol) :-
      tell (Outfile),
     (Protocol = agml, 1, Cp = sgml;
       Caller = server, !, Op = sgml;
        Op = plain),
      (Type - nested, ), } original output form - nested findings
        write('<nested>'), new line(Op),
         write(Fmtlist), new_line(Op), write('</nested>'),
        new line (Op), I
       ),
     (Caller = server,
      write_message(Unfile,Undef,Caller,'<undefined>','</undefined>')
      Caller = exe, Undef \= [],
      write_message(Unfile,Undef,Caller,'***** Undefined Words *****, [] }
     twrite_highlight([],UnSent,Caller)
       true
      ١,
     (Caller - server,
     write('<noperse>'),1,
     write_highlight (Undef, UnSent, Caller).
     write_highlight{[], Pailed, Caller), write('c/noparse>')
     Caller - exe, Errfile \= [], Failed \= [],
     tell (Errfile),
     write('**** Sentences/Phrases Not Parsed ****'), nl,
     twrite_highlight (Undet, UnSent, Caller),
     write_highlight([], Pailed, Caller)
     true
             * no Brrfile to write to
    ١.
% set_args: Process options
```

```
& Argument options
8 p Probfile (Otherwise default is problem massages are not written to file)
§ -i Infile (if input is supplied by file and not standard input
* -m Mode (default is bp; the 6 choices are bp, model - mode5)
t -o Outfile (if output should be file and not standard output)
+ -? Provide list of default arguments
* -pr Protocol - sgml or plain {default is plain!
t -u Undefs (otherwise default is - undefined messages are not written
      to a file)
set args(Args, Mode, Infile, Outfile, Prbfile, Undef, Protocol) :-
      set mode(Args, Mode), set_amount(Args, Amount),
      set protocol (Args, Protocol),
      set infile(Args, Infile), set outfile(Args, Outfile),
      set prbfile (Args, Prbfile) , set_undefs (Args, Undef) .
set mode(Args, Mods) :-
    (nextto('-m',M,Args); nextto(m,M,Args)), !,
    modeis(M, Mode), !.
set_mode( ,bp). * default output type
modeis(relax,mode2) :- !.
modeis(strict,model) :- !.
models(skip, mode4) :- 1.
modeis(longest, mode3) :- 1.
modeis(best,bp) :- !.
models(model,model) :- (.
modeis (mode2, mode2) :- (.
modeis(mode3, mode3) :- !.
modeis(mode4, mode4) :- !.
modeia(mode5, mode5) :- ).
set protocol (Args, Protocol) :-
    {nextto('-pr',Protocol,Args); nextto('pr',Protocol,Args));
     member (Protocol, [sgml, plain]), ).
set_protocol(_,plain).
set_undefs(Arge,Undefe) :-
    nextto('-u', Undefs, Args); nextto(u, Undefs, Args) , !. & undef file option
set undefs{_,[]).
                    % default is no file of undefineds created
set_infile(Args,Infile) :-
    nonvar{Infile}, 1; % Infile is set already
    nextto('-i', Infile, Args), !;
    nextto(i,Infile,Args), !.
set_infile(_,user_input). * default is standard input
set_prbfile(Args,Prbfile) :-
    nextto('-p',Prbfile,Args), !; nextto(p,Prbfile,Args), 1. % prob file option
set_prbfile(_,(]). * default is no file of problems is created
set outfile(Args,Outfile) :-
    nonvar(Outfile), );
                          t Outfile is already set
    nextto('-o',Outfile,Args), 1; nextto(o,Outfile,Args), 1. * outfile option
set_outfile(_,user_output). * default is standard output
new_line(sgml).:- write('<br>'), nl, },
new line(server) :- write('<br>'),nl, !.
new_line(exe) :- nl.
```

```
new_line(plain) :- nl. '
write message([], exe, ) :- !.
write message([], exe, ) :- !.
write message(_, [],plain,_,_} := !.
write_message([],_,plain,_,_} := !.
write_message(File,Contents,Caller,Segmeg,Endmeg) :-
    { member(Caller, [exe, plain]), tell(File), {
    true),
    write(Begmsg), new line(Caller).
    [Contents = []; write list(Contents,1), new line(Caller)
   (Snamey = [], (;
    write(Endmag), !, new_line(Caller)
sentend([X]_],Caller) :-
   member(X,['.',',','?']), new line(Caller), 1.
gettargets([],[]) :- !.
gettargets { [ignore | Rest] , [ignore | Rest] ) : . ! . % possibly ignore info.
gettargets([W1|Rest],(T1|Trest]) :-
     foundword(W1,_,T1), % target for W1
     gettargets (Rest. Trest) , |.
gettargets(W,W). % not in lexicon
isneg(X) :-
    intersect (X, [no,negative, deny, 'rule out']).
writeoutsent([Word(Rest]) :-
  write('''), write(Word), write(''''), !,
  (Word = '''', write(''''), 1; true),
  (Rest \= [], write(','), !, writeoutsent(Rest), !; .
   true), 1.
```

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```
t This file contains predicates associated with SGML tags
   nextTag(+L, Tag, -PreTag, -PostTag) is true if
      L is the starting List
      Tag is an SGML tag; it could be a variable or instantiated already
ŧ
      PreTag is portion of L preceding Tag
      PostTag is portion of L following Tag
nextTag(L, Tag, PreTag, PostTag) :-
    append(PreTag,['c',Tag,'>'|PostTag],L).
t endTag(+L, +Tag, -Pre, -Post) is true if
     L is the starting list
      Tag is the SGML end tag
4
      Pre is the portion of 1 preceding the end of tag
      Post is the portion of L following the end of tag
endTag(L, Tag, Pre, Post) :-
    append((Pre,['<','/',Tag,'>'],Post),L).
t enclosedPart(+L,+Tag,-Enclosed) is true if
      L is the starting List; it is assumed that L is portion of some
      list that follows a begin tag - i.e. 'c', Tag L
٠
      Tag is the 60ML tag
      Enclosed is the portion of text enclosed in tag; not including
      end tag.
enclosedPart(L, Tag, Enclosed, Post) :-
    endTag(L, Tag, Enclosed, Post).
```

```
% file useful.pl - lexical lookup and utility tools
  :-unknown[_,fail].
  :-dynamic (sentence/1).
  :- op(900, fy, (not, once)). % same priority and type as \+
  * useful.pl February 21, 1992
  t preprocess(+S, *B$1, -U, -Sem3, +Mode): preprocesses sentence to
              bracket lexical phrases and remove words/phrases in
              special db of noise words (nosem in asphrase.pl db)
          S is original sentence
  ŧ
  ł
          Bal is preprocessed sentence
  Ł
          U is list of undefined words in sentence
          Mode is mode of process - in skip mode undefined words are removed
            from preprocessed sentence
 preprocess (50, Bs1, U, Sem3, Mode) :- .
                                           3cfnew
_ checkbeg($0,$), % if beginning is 'A)' ignore
    checkphrase (S.Sl.Seml), % bracket all phrases in phrasel lexicon first
   checklist (S1,U1,Bs, Sem2, Mode), & check that all words are in lexicon, remove
   checklist(Bs.U.Bs1,Sem3,Mode). & check for phrases after non-sem are removed
  tappend (Seml. Sem2, Seml).
 tappend (Seml, Sem3, Semlist),
    tunion (U1, U2, U).
  t found checks if word X is defined as a single word, or if X starts a defined
  t phrase
  foundword(X) :-
 \begin{array}{c} \text{wdef}\left(X,\_,\_\right], \ 1. \\ \text{foundword}\left(X\right)^{-}:= \end{array}
      _ semw(X,__,_,),).
 *definition from tagged input
 foundword(X) :-
 phr(X,_,_,), ),
foundword((X|Rest)) :-
        Rest \- ().
      phrasal(X,_,{X{Rest},_), !.
 3/99 added foundword to search the new semact.pl lexicon
 V phrasal using semp was added to util.lp
 1 found/2 returns semantic cat, of word
 foundword(X,Sem) :-
      wdef(X.Sem,_).
 foundword(X.8em) :-
        \operatorname{sem}_{\mathsf{X}}(\mathsf{X},\operatorname{Sem}_{-,-}) .
 tdefinition from tagged input
 foundword (X, Sem) :-
       phr (X, Sem, [],_).
 foundword([X|Rest],Sem) :-
      phrasal(X,Sem, [X|Rest],_).
 % found/3 returns semantic cat, and target form
 foundword (X.Sem. Form :-
      wdef (X, Sem, Form).
 foundword(X,Sem,Form) :-
        semw (K, Sem, Form. ).
 Mdefinition from tagged input
 foundword(X,Sem,Form,_) :-
        phr (X, Sem, [], Form).
 foundword ([X Rest], Sem, Porm) :-
```

```
phresal(X, Sem, (X|Rest], Form).
*collectsem(+Word, -9em): Sem is the list of semantic classes corresponding
    to Word
collectsem (Word, Sem) :-
    setof (X, foundword (Word, X), Sem).
t missing checks if a word present in a centence is defined
-: {X}pmissim
     member(X,S),
     not foundword(X).
t checkbeq(+50,-5) checks beginning of sentence; if it begins with a letter or
& number followed by a ')', that part is skipped
checkbeg((X,')' | Rest] , Rest) :- |.
chackbeg(X,X).
% checks every word in a list to see if it is defined; creates
% a new list of words not defined, and a new list of septence
* where phrases are bracketed.
checklist([),[],[],[],[],[.
Y if X is a list it has already been identified as a phrase in phrasal lex
checklist([X{Rest],Undef,Newrest,Semlist,Mode) :-
     ie liet(X),
     chack_no_sem([X|Rest],Rest1,_],
     checklist (Restl, Undef, Newrest, Semlist, Mode), 1. % is phrase part of nosem
checklist({X|Rest],Undef,(X|Newrest],Gemlist,Mode) :-
     %collectsem(X, Sem),
     is_list(X),
                   X = [W1|Tail],
     phraeal(W1, Sem, X, _),
     checklist (Rest, Undef, Newrest, 9em2, Mode) , (,
     append([Sem], Sem2, Semlist).
checklist([without | Rest] , Undef , Newrest , Semlist , Mode) :-
     checklist({with,no|Rest],Undef,Newrest,Semlist,Mode).
* this problem has to be fixed in preprocessor
T check for a number with a ',' - "11,200" and fix it
tchecklist([X,',',',Y|Rest],Undef,[N|Newrest],[number|Semlist],Mode) :-
     number(K), number(Y), N is X * 1000 + Y, 1,
     checklist(Rest, Undef, Newrest, Semlist, Model, !.
t check for a literal number
                                *cfnew
checklist([X[Rest],Undef,[X[Newrest],(number|Semlist],Wode) :-
     number(X) .
     checklist (Rest, Undef, Newzest, Semlist, Mode), !.
% beginning of List is a preflx of a phrase that is a complete finding
checklist(List,Undef,(Phrase(Newrest),[cfinding(Semlist],Mode) :-
     check_sem_finding(List,Rest,Phrase).
     checklist (Rest, Undef, Newrest, Semlist, Mode) , !.
% beginning of List is a prefix of a phrase that is in nosemantic lexicon
checklist (List, Undef, Newrest, Semlist, Mode) :-
     check_no_sem(List,Rest,Phrase),
     checklist (Rest, Undef, Newrost, Semlist, Mode), ).
beginning of List is a prefix of a phrase that is in phrasel lexicon
chacklist(List, Undef, [Phrase [Newrest], Semlist, Mode) :-
     get_longest_sem(List,Rest,Phrase,Sam),
     tcheck sem(List,Rest,Phrase,Sem), tchange to get longest phrase
     checklist (Rest, Undef, Newrest, Sem2, Mode) , 1,
     append (Sem, Sem2, Semlist).
& beginning of List is a single word that is in semantic lexicon
checklist({X|Rest], Undef,[X|Newrest],Semlist,Mode):-
```

```
collectsem(X,Sem), ),
     tfpundword(X,Sem), !,
     checklist (Rest, Undef, Newrest, Sem2, Mode). !.
     append (Sem, Sem2, Semlist).
& beginning of List is an undefined word
checklist((X|Rest), Undefs, Nrest, Semlist, Mode): .
     checklist (Rest, Undef, Newrest, Semlist, Mode),
     (member (X, Undef) . !: Undefs = (X | Undef) . !),
     (Mode = skip, !, Nreet = NewTest;
      Mode - bpskip, I, Nrest = Newrest;
      Nrest = [X(Newrest)), !
* if beginning is a number followed by a . followed by a non number
's skip;
         scfnew
checkphrase((X,.],(X,.],(]) :- 1.
checkphrase([X,.,2|Rest],Y,Semlist) :-
     number(X), not(number(Z)), checkphrase(Rest,Y,Semlist), ).
t beginning of List is a prefix of a phrase that is a complete finding
t or a phrase in phrasal lexicon
checkphrase(List, (Phrase|Newrest), Semlist) :-
     (check_sem_finding {List, Rest, Phrase), Sem = {cfinding};
      get_longest_sem(List, Rest, Phrase, Sem)
     3. 2.
     %check_pem(List,Rest,Phrase,Sem)), (,
     checkphrase (Rest, Newrest, Sem2) , |,
     append (Sem, Sem2, Semlist).
checkphrase((W|Rest),[W|Newrest],Semlist) :-
     checkphrase (Rest, Newrest, Semlist) .
checkphrase([],[],{]).
check_sem_finding([W|Tail],Tail,W) :-
           W = [W1|Rest], * W is bracketed already
           sem_finding_sent(W1, N, _).
check_sem_finding([W|Tail],Sfinal,Phrase] :-
           sem_finding_sent(W,Phrase,_),
           begsublist (Phrase, [W[Tail], Sfinal), 1.
sem_finding_sent(_,_,) :- fail.
% check_nd_sem(+Sent,-Rest,-Phrase): removes Phrase from Sent resulting
     in Rest if Sent begins with a phrase in nosem (non-semantic list).
check no sem([W[Tail], Gfinal, Phrase] :-
           nosem(W,Phrase), tphrase beg. with W that should be removed
           begsublist (Phrase, [W[Teil], S1),
           remove_comma(81,Sfinal), (. * remove ", " if it is next
tget_longest_sem(+Sent,-Rest,-Phrase,-Sem): Phrase is longest phrase that is
a prefix of Sent; Rest is remainder and Sem is list of semantic classes
get_longest sem{Sent, Rest, Phrase, [Sem]) :-
        setof(X,check_sem(Sent,X),L). % set of Phrases
        maxphrase(L,[],Phrase,D). t Phrase with maximum length append(Phrase,Rest,Sent). t rest of sentence after Phrase
        foundword (Phrase, Sem) .
% check_sem(+Sent, -Rest, -Phrase, -Sem): checks if phrase beginning with
        Sent is in phrasal lexicon: Rest is the remainder of Sent after phrase
        Sem is the semantic class
check_sem{ [W | Tail] , Rest, Phrase, Sem | :-
           phrasal (W. Sem, Phrase, _).
           begsublist (Phrase, [M Tail], Rest).
```

```
% file util.pl
$223234328915834 Utility Predicates 88818837328
fail an unknown predicate
:-unknown(_,fail).
:- op(900, fy, (not,once)). * same priority and type as \+
                               % same priority and type as * or ==
:- op{700, xfx, (\=,==)).
:- dynamic(wfst/6).
: - dynamic (addstotal/1).
:- dynamic(paragno/1).
:- dynamic(sectno/1).
:- dynamic(phr/4).
% wfst(+Rule,+Number,+Res,+Fmt,+60,+S): well-formed symbol table
% White is the name of rule; Number is the option number
        Res is a for success and f for failure
        Fmr is the format (for successes); for failure Fmt is [)
9
        SD is the sentence position at the start of Rule
æ
        S is the sentence position when Rule has been completed
4
         add to wist
addst (Rule, Number, Res, Port, SO. S) :-
   \(\checkst(Rule,Number,Res,Fmt,S0,S)\), $result for rule was saved already \(\checkst(Rule,Number,i,2mt,S0,S)\), $ result from different rule saved
   ( checket(Rule, , Res, Fmt, SO,S). & different rule produced same result
       assert (wfst (Rule, Number, i, Fmt, 60, 5)):
    assert (wfst (Rule, Number, Res, Pmt, SO, S) ;), |.
addst(_,_,_,_,):- !. * always succeed
t checket (+Rule. - Number. - Res. - Pmt. + SO, - S): checke to see if rule has been saved
     in wist
checkst (Rule, Number, Res, Fmt, SO, S) :-
    wfat (Rule, Number, Res, Pmt, So, S).
t beglist (L.Y) - is Y the head of list L
beglist([X]_],Y) := X = Y , !.
v splice(+L1,-L2) : L1 is a list of lists, L2 is merged list
splics(L1,L2) :- append(L1,L2), 1.
tsplice([],[]) :- 1.
*eplice([[]],[]) :- ).
*splice([X],X) :- 1.
tsplice([[][L1],L2] :- eplice(L1,L2),!-
%splice([[[]]|L1],L2) :- splice(L1,L2),!.
tsplice([X][[]]],L) := splice(X,L),!.
tsplice([L1,L2],L3) :-
        append(L1,L2,L3), !.
ŧ
*splice([X[L1],L2) :-
         splice(LL,L3(,
       append(X,L3,L2) , |.
taplicerel - works with relations which have Argl....Argn.
              It splices a Splicelist in each arg of relation
splicarel (Finding, Splicelist, Spliced) :-
             eplice (Splicelist, Sp1),
             (Finding = [rel, X | Rest], spliceargs (Rest, Spl. Sp).
               *splice([[rel,X],Sp],Spliced),!;
```

```
append([rel,x],Sp,Spliced),%;
              splice({Finding, Spl], Spliced) ).
              append(Finding, Spl. Spliced) }.
Aspliceargs - Splices a list into each element of a list
spliceargs([], _,[]) :-i.
spliceargs([Arg1|Rest], Splicelist, Spliced) :-
           *splice([Arg1, Splicelist], Sarg1),
           append(Argl,Splicelist,Sargl),
           spliceargs (Rest.Splicelist.Srest),
           tsplice([[Sargl],Srest],Spliced).
           append((Sargl), Srest, Spliced).
list([],[]),
list([x][)),X}.
list((X|L1), L2) :- list(L1, L3),
                   append([X],L3,L2), !.
% strip(L1, L2) removes extra square brackets from L
strip{[L],L}.
& B is a suffix of A and C is the difference
difflist(A,B,C) :- append(C,B,A).
% S is a sublist at beg. of L if there is a list Rest, which when appended.
    to S results in L.
begsublist(9,L,Rest) :- append(S,Rest,L), ).
% checks that first element in list 9 has semantic category in Semlist
firstword([W1]_],Semlist) :-
    atom(N1), wdef(W1,Sem, ), & semantic category
    member (Sem, Semlist).
firstword([wl|_],Semlist) :-
    is_list(Wil, phrasel(W1,Sem,_,_),
    member (Sem, Semlist).
* removes phrases from first arg that are in asphrase - lexicon of non-sem.
рытазев
remove_по_вей([],[]) :- 1.
remove_no_sem([%|Tail],Sfinal) :-
           nosem(W, Phrase), *phrase beg. with W
           begsublist(Phrase, [N Tail), S1), fremove from scatence
           remove comma($1,82),
                                  %remove "," if it is next
           remove_no_sem($2,$final), t.
remove_no_sem{[W|Tail],Sfinal} :-
           remove_no_sem(Tail,S1),
           append([W],S1,Sfinal) , !.
remove_comma([','|Tail], Tail}.
remove comma(S,S).
* remove_sem(+Sent,-NewSent): Sent is the original sentence, NewSent is
     stripped of all phrases that are defined in lexicon
remove_sem([],[]) :- 1.
remove_sem(S,NewS) :-
    check_sem($,Rest,_,_), * phrase in sent. is in lexicon - remove it
    remove sem (Rest, NewS) , !.
remove_sem(8,NewS) :-
    chack_no_sem($,Rest,_},
                            t phrase in sent, is in nosem list - remove it
    remove_sem (Rest, News) , |.
remove_sem[[X[Tail],[X[MewS]] :-
    remove_sem(Tail, NewS), 1. % not a phrase, process rest
* remove words(+Sent,-NewSent): Sent is the original sentence, NewSent
    is stripped of all words that are in lexicon
```

```
remove_words{[], {]} :- |.
remove_words([X|Rest],NewRest) :-
    ( (foundword(X); number(X));
                                    & X is defined in lexicon
       remove_words(Rest,NewRest) .!;
       remove_words(Rest,New), NewRest = [X|New), } % X is not in lexicon
*maxphrase(+ListofPhrases.+Maxin,-MaxQut,InitMaxLen) is true if
    ListofPhrase is a list of multi-word phrases,
      Maxim is phrase with maximum words so far
      MaxOut is phrace with maximum length of phraces in ListofPhraces
      InitMaxLen is length of initial phrase which is of max. length
maxphrase([), Maxin, Maxin, _) := :. % no more phrases - maximum is same as maxin
maxphrase([P|Rest], Maxin, Maxout, InitMaxLen] :-
     length (P, Len), & length of first phrase
     ( Len > InitMaxLen, ), maxphrase(Rest,P,Maxout,Len);
       Len c InitMaxLen, (, maxphrase (Rest, Maxin, Maxout, InitMaxLen)
     }.
facclex(Sem, W,SD,S) :-
    outputform(htext), !, acclex1(Sem, W, SO, S).
acclex(Sem, W, SO, S) :-
   acclex2 (Sem. W.SO, S).
acclex(Sem, W, SD, S) :-
   acclexes (Sem, Syn, Target, Features, SO, S).
& check lexicon for word or physic, Target form is original W
acclex1(p,[P,C],[W|Rest],Rest) :-
         is list(W),
         find_sem_phrase(p, [F, C], W).
acclex1(p,[P,C],[W|S],S) :- atom(W),
                            wdef(W, p, \{P, C\}).
acclex1(Sem, [W], [W-Rest], Rest) : .
         is_list(W), %if bracketed list, get Sem and Code from phrasal lexicon
         find_sem_phrase(Sem,_,W).
acclex1 (8em, W, [W|S], S) :-
                          wdef (W, Sem, _ } .
* check lexicon for word or phrase, Target form is taken from lexicon
lacclex8 (Sem, Code, [W Rest], Rest] :-
         is_list(W), Wif bracketed list, get Sem and Code from phrasal lexicon
          find sem phrase (Sem, Code, W).
acclex2(Sem,Code,[W|S],S):- foundword(W,Sem,Code),
                                            nonvar (Code) .
                                                             % protect against
lex. error
t find a phrase [W|Tail] in lexicon that begins with W and has category Sem
find_sem_phrass(Sem,Code, [W|Tail]) :-
        phrasal(W, Sem, [W[Tail], Code); * phrase and code beg, with W
        nonvar (Code) .
t case where phrase is already bracketed, look up phrase
sem_finding_phrase1(Code,[W[Tail],Tail) :-
         is_list(W), tphrase is bracketed
        find_sem_sent(Code,W),
         nonvar(Code).
                         *protect against lexical error
t case where phrase is already bracketed, look up phrase
sem_finding_phrase2(Code,[W{Tail],Tail) :-
         is list (W), aphrase is bracketed
```

```
find sem_sent(Code,W),
          nonvar(Code). *protect against lexical error
* Phrasal succeeds if lexicon contains phrase
phrasal (W1, Sem, Phrase, Code) :-
       phrase (W1, Sem, Phrase, Code, ). %multi-word phrase in lexicon
t added Warch15, 1999
phrasal (W1, Sem, Phrase, Code) :-
            semp (M1, Sem, Phrase, Code, Features) .
Y lexical definition from marked up imput
phrasal(W1,Sem,[W1|Tail],Code) :-
            phr (W1, Sem, Tail, Code) .
acclexas(Sem, Syn, Target, Features, [N|S],S):-
            atom(W).
            somw (W. Sem, Target, Peatures),
            gynw(W. Synclass).
            member (Synclass, Syn).
acclexes (Sem, Syn, Target, Features, [W S], S]: -
            is list (W),
            find phrasess (W, Sem, Syn, Target, Features).
find phrasess ([W1 | Tail], Sem, Syn, Target, Features) :-
            semp (W1, Sem, [W1 | Tail] , Target, Features) ,
            symp(W1, [W1|Tail],Symclass),
            member (Synclass, 6yn).
t lexical definition of a complete finding
find sem sent (Code, (W|Tail)) :-
         sem_finding_sent(W,[W|Tail],Code).
listify(c,[c]) :-
         atom(C), I.
listify(C,C) :-
          is list(C), I.
% distributes left mods and right mods over list of findings creating
t list of lists of findings with mods
distributemods([],[],_,_,_) := |.
distributemods(Dist, [D1 Twil), Lmode, Rmode, Type) :-
       distributemods (Dist2, Tail, Lmods, Rmods, Type), %distributed for remainder
        mergemods (Lmods, Rmods, Allmods),
        frame (D, Type, D1, Allmode), tType frame with mods
        append((D).Dist2.Dist).
                                    * Combine findings to get list of findings
* fixconj - if Leftmods has [certainty,no], and Conj = or, change Conj to and.
        no A or B = no A and no B; 'denies A,B, or C' is similar.
fixconj(Leftmods,Conj,[rel,and]) :-
         {member([certainty,no],Leftmode); member([certainty,deny],Leftmode));
        Conj = [rel, ar].
fixconj( ,Conj,Conj).
         write sentences/1 inputs a PROLOG list and prints out lines
         which which are English sentences. No wrapping is done.
write_sentences(()) :- 1.
write sentences([X]) :- write(X), nl. % special sentence - section name
write_sentences(['<',p,'/','>'}) :-
     write(''), nl.
                           & paragraph mark
write sentences([X|Rest]) :-
        upper_first((X|Rest),(U|Rest)),
```

```
write(U), t First letter of first word made upper case
        IX = U, chaforpunct(D, Rest), |, write_terms(Rest); % no space needed
        write(' '), write terms(Rest)
         write_sentence/2 inputs a PROLOG list and prints out an English
         sentence wrapped. Idlen is the starting position of the sentence
ŧ
         in the output.
          uses libraries ctypes, basic, not
write sentence([X[Rest], Idlen) :-
    upper first([X|Rest], [U|Rest]),
    wrice (U),
    name (U, LU), length (LU, L),
    (U = X, chkforpunct(U,Rest), !, write_terms(Rest, L+Idlen);
     write(' '), write_terms(Rest, L+Idlen+1)
    ١.
        write list inputs a PROLOG list and prints out a sentence like list.
         wrapped. Idlen is the starting position of the list in the output.
write_list{[X|Rest],Idlen) :-
    write(XI,
    name (K. LU), length (LU, L),
   ( chkforpunct(%,Rest), write_terms(Rest, L+Idlen), !;
     write(' '), write terms(Rest, L+Idlen+1)).
twrite_list(+List, +Idlen, -Idlenout)
a write list prints out a sentence like list with wrapping if necessary.
    List is the list to be printed
    Idlen is the column position at start
    Idlenout is the column position at end
write_list({},Len,Len) :- !.
write_ligt({X |Rest}, Idlen, Idlenout) :-
    acomic(X), write(X),
    name(X,LU), length(LU,L),
    (L + Idlen > 74, nl, Idlen2 = 1, !;
     Idlen2 - L + Idlen, |
    1.
  (chkforpunct(X,Rest), write_list(Rest,Idlen2,Idlenout). !;
    write(' '), write list{Rest,L+Idlen2+1,Idlenout}, !
   is_list(X), write_list(X,Idlen,Idlen2), write_list(Rest,Idlen2,Idlenout).
upper_first([X[Rest], [U[Rest]]:-
     name(X, [L[Z]).
 (is alpha(L), Up is L - 32, !; Up = L),
 name (U, (Up[2]), L
% write_terms/1 writes out a word followed by blank, except for punctuations.
write_terms([]) :- |.
t case where X is and of sentence
write terms { [X | Rest] ) :-
   (X = {}^{t}, {}^{t}, X = {}^{t}; {}^{t}), t last word of sentence
   write(X), nl, !, write_sentences(Rest), !.
Y case where K is interior of sentence
write_terms([K|Rest]) :-
     write(X),
     (chkforpunct(X,Rest), write_terms(Rest);
```

```
write(' '), write_terms(Rest)
      ), 1,
* write_terms(List, Used); writes the terms in list and counts the number
        of columns used; starts new line if 75 columns have been used
write_terms([),_) :- |.
& at end of list
write_terms((.1, _} :- write('.'), n1,!.
write_terms([;],_} :- write(';'), q1,!.
X is a punctuation, don't add to final count
write_terms({X|R},Used) :-
   ( R = [], write(' '), write(X), ';
    chkforpunct(X,R),
    write(X), write terms(R, Used), !
  ).
* X 18 last word in sentence
write_terms([K,.], Used):-
   pame(X, List), length(List, Len),
   Need is Len + 2,
   Total is Used + Need.
    (Total =< 75, write(' '), write(K), write(.);
    Total > 75, 01, write(' '), write(X), write(.)),
   nl, !.
X is last word in sentence
writs_terms([X,;], Used):-
   name (X, List), length (List, Len),
   Need is Len + 2.
   Total is Used + Reed,
    (Total =< 75, write(' '), write(X), write(';');</pre>
    Total > 75, nl, write(* '), write(X), write(.)),
   nl, I.
* X is followed by ','
write_terms([X,1,1]Rest], Used]:-
    name(X, List), length[List, Len],
   Need is Len + 2,
   Total is Used + Need,
   (Total =< 75, write(' '), write(X), write(','),
    write_terms(Rest, Total);
    Total > 75, nl, write(' '}, write(X), write(','),
    New is Need - 1, write_terms(Rest, New}),
t writes blank + name of X, used is length of name+1
write_terms([x|Rest], Vsed):-
   name (X, List), length (List, Len),
   Need is Len + 1,
   Total is Used + Need,
   [Total =< 75, write(' '), write(X), write_terms(Rest, Total);
Total > 75, nl, write(' '), write(X), write_terms(Rest, Len)},...
write terms(['X,''s'|Rest], Used):-
   name(X, List), length(List, Len),
   Need is Len + 3,
   Total is Used + Need,
   {Total =< 75, write(' '), write(X), write("'s"),
    write terms (Rest, Total);
    Total > 75, nl, write(X), write_terms(Rest, Len)), |.
t processes sentences in Infile; writes formate to outfile
Bentances beginning with '8' are treated as comments
testaenta (Infile, Outfile) :-
```

```
see (Infile), seen, see (Infile).
    tell(Outfile),
   readtests.
    see (Infile), seen, told.
% reads next sentence and processes it
readtests :-
    read in (X),
    (X = and of file. !!
    x = \{eoff, [.]\}, !;
     X - (**), (7
     X = ['%']_], !, readtests; % don't process comments
    preprocess (X, Bs, Undef, Semlist, skip),
    ( Undef = [],
     dosent(X,Bs,Semlist,Pmt,Messagt,impression,W,chestxray,strict,0).
     write sentence(X,1), write(85), nl,
     write(Fmt), nl;
     Undef \= [], write_sentence(X,1), write(Bs), nl, write(Undef|, nl),
                  & read next sentence
     readtests
% Reads in all sentences from input file and creates one list of all sentences
get_inputsents(Prevlist, Toklist) :-
    read in (X),
     (X = snd_of file, Toklist = Prevlist, !;
     X = [eoff, ...], Toklist = Prevlist, !;
     X = [''], Toklist = Prevlist, !:
      (last('',X), append(Toxlist,[''],X], !;
                                                *remove
       append (Prevlist, X, Newlist),
       get_inputsents(Newlist, Toklist)
      }).
*get sentence(+A, -B, -C)
t Gers next sentence from input list containing all sentences read in
& Don't end a sentence if "." is preceded by a number and followed by
% a number and unit measure - 1.25 cm, 1.5 cm, .5 cm
t or is followed by s "." which is part of abbreviation
* get_sentence(A, B,C) - A is list of all sentences in report.
                      - B is list containing one sentence
                      - C is remainder excluding B
* sgml tag for multi-word phrase containing '.' that is not end of sentence
get sentence(('<',phr|Tail), Sentence, LRost) :-
        enclosedPart(Tail,phr, Between, Rem), & Between beg. part of open phr and
close tag of phr
      attribute
      (MoreAttributes = ['>'[Phrase], TargetList = Phrase, !;
       MoreAttributes = (t,-,'''|TargetPlus), % Target terms plus end of phr
       append (TargetList, [ "" , "> | Phrase), TargetPlus), } } t t attribute followed
by actual phrase
      Phrase - [W1 Rest],
      append (Phrase, Sest, Sestence) ,
      concat atom(TargetList, Target),
      assert (phr (W1, Sem, Rest, Target)). & assert lex def according to input
        %Phrase = [W1|PRest].
        Wabbrev(W1, [W1 | PRest), Target, _),
        get sentence (Rem, SRept, LRest), 1.
```

```
t Ignore sentence starting with 'f', get next sentence
get_mentence(['%','%' Rest], Sent, Remainder) :-
     get_sentence(Rest,_,Rem),
     get_sentence(Ram, Sent, Remainder).
get_sentence{[X,.,Y,Z]Rest],[X,.],[Y,Z]Rest]) :- Y break up "140. 3+"
    number \{X\}, number \{Y\}, y = 1+1, y = 1+1 belongs to y = 1+1 for new sentence
get_sentence([X,.,Y,Z{Rost],[N|SRest],LRest):-
      number(X), number(Y),
      t(wdef(Z,unit,_); Z = x).
      ١,
      name(X,D1), name(.,D2), name(Y,D3), name(B+00',D4),
      append([D],D2,D3,D4],D), name(N,D), Y put number together
      get_sentence([2|Rest], SRest, LRest).
* common abbrev
get Bentence { [X, . | Rest] , [X | SRest] , LRtst | :-
                                                % abbrev ending in "."
t list of common abbreviations seen in reports should not end sentence
   member(K, [vs.dr.cm.mg]), get_sentence(Rest, SRest, LRest), i.
t list of start of names in reports should not end sentence
get Bentence([X, , Rest], [X|SRest], LRest) :-
                                                % abbrev ending in "."
   member (X, [ms, mr, mrs, dr, st]),
   skipname (Rest, Rest0),
                          * skip name part
   get sentence(RestO, SRest, LRest), !.
* more known abbreviations
get_sentence((N1 | Rest), [Rep | SRest], LRest) :-
     abbrevchk([W1|Rest],_,Rem,Rep), & abbreviation
     gst_sentence(Rem, SRest, LRest), !.
& possible simple xml tag for new paragraph
get_sentence(['<',p,'/','>'|Resi],Sent,Reml :- %skip paragraph warker
    get sentance (Rest, Sent, Rem) , 1.
% xml tag for sentence '<8>'
get_sentence {['<',s,'>'|Tail], Sentence, Rest) :-
      enclosedPart(Tail,s,Sent,Rest),
       {last('.', Sent), Sentence = Sent, !; talready has '.'
      append (Sent, [.], Sentence)
      ), 1,-
                     tadd '.'
get sentence([.(Rest],[.).Rest) :- 1. tend of a sentence
get_sentence([; Rest],[;),Rest) :- !.
t interior of sentence
get_sentence([x|Rest],[x|SRest],LRest) :-
                       get_sentence(Rest, SRest, LRest).
get_sentence({[], {[], []}).
                          v no more ≤entences
t abbrevchk(+WordList,-ApList,-RemList,-Target) is true if an abbrev is prefix
   of WordList, RemList is suffix of WordList (excluding prefix),
    Ablist is prefix consisting of abbreviation
    and Target is target form of abbreviation
abbrevchk([W1 Rest], AbList, RomList, Target) :-
     abbrev (W1,AbList,Target,Dom). % abbrev knowledge base indexed by 1st word
     append(Abbist.Rem,[W1 |Rest]), % remainder of abbrev. must be in sontence
     {Dom = general, !;
                          % abbrev. Applies to all domains
      domain (Thisrep), Dom = Thisrap, !: % abbrav, applies to this domain
      is_list(Dom), member(Thisrep,Dom) % this domain in abbrev. list
     1.
     ( % add back '.' to sentence if it also signals end of sentence
      Rem = [], last('.', AbList), Remlist = ['.'], | %no more words
      ; Y words that generally start a new sentence
```

```
Rem = [W2]_], last('.',AbList), member(W2,[his,her,he,she,the,this)),
         RemList = ['.'[Rem], !
         ; * don't add '. ' back
       RemList = Rem
     1.
skipname(+Beglist,-Endlist): skips next word after "mr" or "st"
skicname([],[]] :-!.
skipname([0,''', |Rest], Rest):- !. % "O'Grady
ekipname([_{Rest],Rest) :- !..
Sget section (+Toklist, -Sents, -Rest, -Section, -Printname, Addno)
* Toklist contains input list; 1st sentence should be a header;
* Sents are all sentences in section; Section is name of section
% Sentences at beg. of Toxlist are ignores until a section beader is found
get_section([T|Toklist], Sents, Rest, Section, Printneme, Addno) :-
       * first sentence should be section header
      get sentence([T|Toklist], Sentence, RToklist),
      (section_header(Septence, Rsent, Section, Printneme), % Septence is a section
header
       append (Rsent, RToklist, RToklist2),
       get_sectionsents(RToklistZ,Sents,Rest),
       (Addno = 0, !; % testing if input begins with section header
        Addno - 1. ! , sectno (Sectno) , Newmo is Sectno + 1,
        retractall(sectno()), assert(sectno(Newno))
       retractall(paragno(_)), assert(paragno(1)), %ist parag. of section
                                                  tist sentence of parag.
       retractall [sentno(_)}, assert(sentno(0)}
       ; % lat sentence is not a legitimate header - return []
        Section - [] .
       % get_section(RToklist, Sents, Rest, Section) % skip till find header
get_section([], [], [], [], _,_),
get_sectionsents([], [], []) :-!.
get sectionsents(Toklist,Slist,Rest) :-
     get_sentence(Toklist,Sentence,RToklist), % one sentence
     ( - section_header(Gentonce, _ , _ ) , twore sentences in section
        get sectionsents (RToklist, RSents, Rest),
        append (Sentence, RSenta, Slist)
       ; I the next section is a section header - return
      Rest - Toklist, Slist = []).
section_header(S,RestS,'report clinical information item',
          'CLINICAL INFORMATION: ,') :-
    ($ = [elinical,information,':','.'], !, RestS = [];
     begaublist([clinical,information,':'],S,RestS), !,
     S = [clininfo,':','.'], Rest3 = {], |;
     begaublist ([clininfo, ':'], S, RestS), |
section_header{S,RestS, 'report impression item',
            'IMPRESSION:.') :-
   (S = [impression, ': ', ], RestS = [], !;
    begaublist ([impression, ':'), S, RestS), !
section_header(S,Rest,'report summary item','SUMMARY:.') :-
    8 = [summary, ': Rest].
```

```
section_header(S.Rest8, 'report description item', 'DESCRIPTION: .') :-
   (S = [description, ':', .), RestS = [], 1;
    begaublist ([description, ':'], S. RestS), 1
   ١.
section header(S,Rest,'report diagnosis item','DISCHARGE DIAGNOSIS:.') :-
   [6 = [discharge, diagnosis, ': '|Rest] ;
    S = [final, diagnosis, ': '[Rest];
    S = [principle, diagnosis, ':'|Rest]; S = [associated, diagnosis, ':'|Rest];
    S = [transfer,diagnosis,':'[Rest];
    6 = [diagnosis,'(',es,')',';'|Rest];
    S = [diagnosis,: |Rest]
   ), !.
section_header(5, Rest.'report laboratory data item(,'LAB DATA:.') :-
    S = [laboratory,data,':'|Rest), !.
section_header(8,Rost,'report medications item','MEDICATIONS:.') :-
    S = [medications,': |Rest], ).
section header(S,Rest,'report current medications item','MEDICATIONS:.') :-
    S = [current, medications, ': 'Rest], |.
section_header($,Rest,'report discharge medications item',
        'DISCHARGE MEDICATIONS:.') :-
    S = [discharge, medications, ': | Rest], }.
section header(9,Rest, 'report discharge disposition item',
     'DISCHARGE DISPOSITION: .') :-
    S - [discharge, disposition, ': '|Rest], !.
section_header(S.Rest, 'report medications on admission item',
     'MEDICATIONS: . ') :-
    8 = [medications.on,admission,';'|Rest], ).
section header(S.Rest. 'report medications on transfer iterm',
     'MEDICATIONS: .') :-
     8 = [medications,on,transfer,':'|Rest], !.
section_header(S,Rest,'report procedure item','PROCEDURE:.') :-
  (S = [operation,':'|Rest]; S = [procedure,':'|Rest]
section_header(S,Rest,'report indications for procedure item','INDICATION8:.')
  (S = [indications, for, procedure, ': '[Rest], S =
(indications, for, operation, ': ' | Rest)
  ł,
   .
section_header{S,Rest,'report preoperative diagnosis item','PREOP DIAGNOSIS:.')
   S = [preoperative.diagnosis,':'[Rest], [.
section header (8. Rest. 'report admitting diagnosis item', 'ADMITTING
DIAGNOSIS: . ');-
   S - [admitting, diagnosis, ': '[Rest], !..
section header(8, Rest, 'report postoperative diagnosis item', 'DIAGMOSIS:.') :-
   S = [postopsrative, diagnosis,':'[Rest], {.
section_header(8,Rest, 'report physical examination item',
        'PHYSICAL EXAM: . ' ] :-
   9 = [physical,examination,':'|Rest], !.
section_header(S,Rest, 'report chief complaint item', 'CHIEF COMPLAINT: .') :-
   S = [chief,complaint, ': '[Rest], 1.
section_header(S.Rest,'report hospital course item','ROSPITAL COURSE:.') :-
   S = [hospital,course, ': | Rest], !.
```

```
section_header(S.Rest,'report allergy item','ALLERGIES:.') :-
    S = [allergies, ': | Rest] . (.
section_header(S,Rest,'report follow up item','FOLLOW UP: ') :-
   S = [follow, up, ': ' | Rest], 1,
section_header(S.Rest, 'report findings item', 'FINDINGS:.') :-
   S = [findings,': | Rest], !.
section_header(S.Rest,'report indications and findings item','FINDINGS:.'| :-
   S = (indications, and, findings, ': '[Rest], ).
section_keader(3,Rest,'report indications and findings item','INDICATIONS:.') :-
   S = [indications, ': | Rest], !.
section_header(5,Rest,'report provisional diagnosis item','PRELIM DIAGNOSIS:.')
   S = [provisional, diagnosis, ': 'Rest), !.
section_beader(S,Rest,'report review of systems item','REVIEW OF SYSTEMS: ') :-
   S = [review, of. systems, ': 'Rest], !.
section_header{S,Rest,'report past history item','PAST MEDICAL HISTORY:.') :-
   5 = [past, history, section, ': 'Rest], !.
section_header(6,Rest,'report past history item','PAST MEDICAL RISTORY:.') :-
   S = [past,medical,history,':'|Rest], !,
section_header(S,Rest,'report social history item','SOCIAL HISTORY:.') :-
   S = [social, history, ': '| Rest], 1.
section_header(S,Rest,'report past history item','PAST MEDICAL HISTORY: '] ;-
 · Ω = [history, ': '[Rest], 1.
section_header(S,Rest,'report past bistory item','PAST MEDICAL HISTORY:.'} :-
   S = [brief, history, ': ' | Rest], 1.
section_header(S.Rest, 'report history of present illness item',
          'HISTORY OF PRESENT ILLMESS: .') :-
   S = [history,of,present,illness,':'[Rest], !.
scotion_header(S,Rest,'report history of present illness item';
          'HISTORY OF PRESENT ILLMESS: . ') ;-
   S = [history.of,the.present,illness,':'|Rest], |.
section_header(S,Rest,'report specimen item','SPECIMEN') :-
   S - [specimen | Rest], 1.
sentence consists of id number only or "." only.
isidentifier([X,.]) :-
        integer(x).
ieidentifier([X,;]) ;
        integer(X).
isidentifier([.]) :- ). * sentence consists only of .
isidentifier(['.','4808>']) :- !.
isidentifier(('<',p,'/','>')) :- * paragraph marker sentence - update no. -
       paragno(N),
       retractall(paragno(_)),
       Newno is N + 1,
       assert (paragno (Newno)),
       retractall (sentes( ) } .
       assert (sentno (0)).
* tripsentence is true, if sentence should be ignored.
* Skip sentences containing family info
skipsentence([xj_3) ;-
   foundword(X, family), 1.
akipsentence((%}_)) :-
   foundword (X, incurance) | |.
* This occurs if sentence contains
```

```
t a sequence in skips database and sentence also contains findings.
 skipsentence([X[Rest],Semlist,Error) :-
    skips([X|6seq]), & X is the beg. of subseq. in skip database
    prefix([K|Rest],[X|Sseq]), & sentence contains subseq.
     (Subtype(_,Semlist), & sentence contains information to be extracted
     Error - no; * don't try to segment
     Error • yes}, !.
                        % treat sentence as error and try to segment.
 skipsentence([_|Rest].Semlist.Error] :-
    skipsentence(Rest, Semlist, Error).
 % findingseg(+S,~Fseg,-Begseg): partitions sentence
         S is the sentence; Begseg is the segment preceding the
           modifiers of the finding: Feeg is the segment of 6 starting
           with the leftmost modifier of the finding and consists of the
           remaining sentence.
 findingseg{S,Fseg,Begseg} :-
     partition(S, Begpart, Restpart),
     (Begpart - [], Begseg - [];
      Restpart = [], Faeg = [], Begseg • S;
     rightlatmod(Begpart, Begseg, Modseg)),
     append (Modeeg, Restpart, Pseg).
 findingseg(_,[], _) :- 1.
 actionfindingseg(S.Fseg, Begsag):-
       partition(S, Begpart, Restpart),
      (Begpart = [], Begseg = [];
      Restpart = {], Fmeq = [], Begseg = S;
       reverse (Bagpart, ReversedBefore),
           findsubstance(ReversedBefore, Rest),
           append (Substancepart, Rest, ReversedBefore),
           reverse (Substancepart, Leftpart),
         reverse (Rest, Begseg) ,
       append(Leftpart,Restpart,Fseg)).
 actionfindingseg(_,{],_) :- |.
 findaubstance(([, [)):- !,
 findsubstance([X Rest], Rest); -
       substance( , [x] , {} } , ) .
 findsubstance([X Rest1], Rest):-
       findsubstance [Rest1, Rest] .
 † partition(+S,-Begpart,-Restpart): partitions sentence
         S is initial
 * partition(+8, -Begpart, -Restpart): partitione sentence
         3 is initial sentence; Begpart is part of sentence before the
· •
           finding; Restpart is the rest of the sentence and starts with
           the finding. If there are 2 consecutive findings
           the lat one is considered a modifier
 partition([),[],(]) :- !.
 partition([X|Rest], [X|Begpart], Restpart] :-
     not(isfinding(X)), |, partition(Rest, Begpart, Restpart).
 partition([X,Y|Rest],[X],[Y|Rest]) :-
     isfinding(X), isfinding(Y), |.
 partition([X|Rest],[],[X{Rest]) :-
     isfinding(X), (.
 * isfinding(+X): is true if X is a word or phrase whose semantic class
         is a finding or subtype of finding.
```

```
isfinding(X) :-
           foundword (X, Sem),
                                                   * semantic class of word
                                                        % is class a type of finding, recommend, or technique
           subtype(_,[Sem]),
& semantic class which are types of relevant information
Bubtype(finding,Sem) :-
           intersect (Sem, [attach, createbond, breakbond, activate,
             inactivate, substitute, transcribe, express, promote,
             signal]].
 % there is only one type of technique class
subtype (technique, Sem) : .
           member (technique, Sem) .
subtype(time,Sem) :-
           intersect (Sem. [status, sstatus, change, tmper, vetatus] ) .
findinginlist(Sem) :-
         intersect(Sem, [attach, createbond, breakbond, activate,
             inactivate, substitute, transcribe, express, gromote,
             signal]).
% chkforpunct(+W,+Rest): is true if there should be no space after word W
& nothing left to write.
chkforpunct(W,[]) :-!.
t is true if there should be no space before word after current word
chkforpunct(_,[W|_]) :-
      ispunct(W).
* ispunct(+W) is true if W is a punctuation for sentence print out
t The following characters are not treated as punct: - `#$ ^ & *
\{\{i,i\},i,i,i\},\{i,i\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i,j\},\{i
& rightletmod(List, Firstpart, Modpart): Modpart begins with the first
        word in List which is a modifier; Pirstpart are the preceding words
right1stmod([],[),[]} :- 1.
% X is a modifier or finding; Beginning part is empty
rightlatmod([X{Rest],[],[X|Rest]) :-
      foundword(X, Sem, Target),
       {modifier(Sem); Sem = p, Target - [ .conn]; subtype(_,(Sem])}, :.
* X is not a modifier or finding
rightletmod([X|Rest],[X|Firstpart],Modpart) :-
      rightlstmod(Rest,Firstpart,Modpart).
frame(Frame, Type, Value, Mode): creates a list Frame, whose 1st
                 element is Type, 2nd element is Value, and 3rd is a list of
4
                 modifier frames or is emtpy
8
& Case where modifier list is empty; Value should be atom except for
certain types;
frame((Type, Value), Type, Value, X) :-
         \{X = \{\}; X = \{\}\}\},\
         atom(Value), !.
3 Special cases where value of type should be a list
frame([Type, [H[R]], Type, [H[R], X) :-
                (x = \{\}; x = (\{\}\}),
               oklist(Type), !.
% Modifier list is merged with list consisting of Type and Value
frame(Frame, Type, Value, Mods) :-
           atom(Value).
           append([Type, Value], Mods, Frame), !.
```

```
frame (Frame, Type, [K|R], Mods);-
      is list(R),
      append (R, Mods, NewMods).
      append([Type, R], NewMods, Frame), !.
 & Components of Frame
 frame([Type, Value | Mode) | Type, Value, Mode) :- ].
 % Value of Type should not be a list; first element of value is real value
 frame([Type, R. Rest], Type, [8 | Rest], []) :- |.
 § Special cases where value of type should be a list
 f(x) = \frac{1}{2} (x)^2. Type, f(x) = \frac{1}{2} (x)^2.
     oklist(Type), !.
 Y Value of Type should not be a list; first element of value is real value
 frame(Frame, Type, (H|Rest), Mods) :-
     mergemods (Rest, Mods, NewMods),
     append{[Type, H], NewMods, Frame),
 * mergenodinf[-F,+frame,+Mods): Frame is a type-value-mod frame; Mods
     is an additional set of modifiers for Frame; mergemodinf adds Mods
     to Frame, resulting in F.
 mergemodinf({],[],_):-1.
 margemodinf(F,[rel,X|Rest],Modrel):-
         mergemodinf(Pl, Rest, Modrel),
         append([rel,X),Fi,F),!.
- mergemodinf(P,[F1,X|Modfin],Modrel):-
         atom(f1), mergemods [Modrel, Modfin, Mod),
         append([F1,X),Mod,F], |,
mergemedinf[F,[K|R],Modrel):-
        mergemodinf(F1,K,Modrel),
         mergemodinf(F2,R,Modrel),
         append([F1],F2,F),
 * addmodstof(+Args,+Mods,-NewArgs) is true if Args is a list of formats.
 * Mods is a list of modifiers and NewArgs is a list of formate where Mods
 t has been added to modifier list of that format
 addmodstof([], ,[]) :- |, % no more formats
addmodstof([Format1|Rest],Mods,[F1|NewRest]) :-
        mergemodinf(F1,Format1,Mods). * merge modifiers into lst format
        addmodstof(Rest, Mods, NewRest), 1. %add modifier to remaining
t oklist(+Type): is true if Type can have a list as its value
oklist (unitval).
oklist[age].
oklist (measure) .
oklist(prev_timeunit).
oklist (future_exam) .
* mergemods(+Mods1,+Mods2,-Mod): Model and Mods2 are a list of modifier lists
*
         Mod is the marged list; some elements of Mods! and Mods2 may be
*
         empty
mergemods([], M, M) :- !.
mergemods (M, [], M).
mergemods (Mods1, Mods2, Mod) :-
         delete(Modal,(),M1),
         delets (Mods2, [], M2),
         append(M1,M2,Mod).
addmod(+Mod,+Modlist,-NewMod): NewMod is formed by including
        Mod into Modlist
. [-: (bow,bod,[]) hombas
```

```
asdmod (Mod, [], [Mod]) : - 1.
addmod(Mod, Modlist, NewMod) : .
   app nd([Mod], Modlist, NewMod).
% modlist(+ListofMods,-Mods): ListofMods is a list consisting of
    individual modifier frames, some of which may be empty
    Mods is formed as a list of non-empty modifiers
modlist{[],[]} :- !.
f ignors a modifier which is an empty list
modlist[[[]]R], Mode) :-
    modlist(R.Mods), 1.
-: (accom, [SR] [RR]] mocks) :-
    atom(H), 1,
    modlist (R2, Rmods),
    addmod([X|R1],Rmpds,Mods).
modlist([[H|R1]|R2], Mods) :-
    is_list(H), !, % is first element is a list
    modlist (R2, Rmode).
    mergemoda([H|R1], Rmods, Mods).
%bpframe: creates from for sequences of bodyloc/region/position
bpframe(F,[], Type, Bp1, Bp2) :- % no conj relation but more than 1 bodyloc
        frame (Bpl, EpiType, EpiVal, EpiMode). %contents of Epi frame
        frame (Bp2, Bp2Type, Bp2Val, Bp2Mods), %contents of Bp2 frame
        ( {EplType = region; BplType = position),
         Bp2Type - hodyloc, % 'left lung', 'area of lung' mergemode (Sp1Mods, Sp2Mods, SpMods), %now region modifier
         frame (NawBp2Mods, Bp1Type, Bp1Val, BpMods), anew Bp1 frame w new mod
                                                 t main frame is bodyloc
         frame (F, Bp2Type, Bp2Val, [NewBp2Mods])
         SpiType = bodyloc, Bp2Type = bodyloc, Type = main, %Sp2 is main
         mergemods(Bp1Mode, Bp2Mode, BpMode), thew bodyloc modifier
         frame (NewBp2Mods, Ep1Type, Bp1Val, BpMods), % 'joint of shoulder'
         frame (F, Sp2Type, Bp2Val, [NewSp2Mods])
                                                      t main bp frame is shoulder
         mergemods (BplMods, Bp2Mods, BpMods).
         frame (NewBpiMods, Bp2Typs, Bp2Val, BpMods), & 'shoulder joint'
                                                      Y main by frame is shoulder
         frame(F, Bp1Type, Bp1Val, [NewBp1Mode])
        1. 1.
opframe (F.Rel,_, Spi, Sp2) :- * no conj relation but more than i bodyloc
        Rel = (rel,Conj|_), 8p2 \= [],
        mergemode ([Sp1], [Bp2), Conjarge).
        frame (F, rel, Conj, Conjarge).
getrelation (R, Fl, F2, F) :-
        (F2 \= [],
            (F1 = [rel,Conj1]Resti], R = [rel,Conj],
                                     {Conj1 = '.'; Conj1 = or: Conj1 = and},
                                     (Conj = ','; Conj = or; Conj = and);
              Rest1 - [F1]},
            {F2 = [rel,Conj2|Rest2],
                                     (Conj2 = 1, 1; Conj2 = or; Conj2 = and);
              Rest2 \Rightarrow [F2] \rangle
            %splice([R, Restl, Rest2], F);
             append([R,Rest1,Rest2],F);
          P2 = [], P = F1 ).
```

```
uptotal :-
   addstotal(X),
   X =< 50,
   NewX is X + 1,
   rstractall(addstotal(X)),
   assert(addstotal(NewX]), ).</pre>
```

.

Appendix E .

\$88V8('8'}='AAAC'; \$Bave { 'D'}= 'AAAG'; \$sev={'c'}='AAAT'; seave{'d'}='AACC'; \$8ave{'c'}='AACG'; Ssave {'f'}='AACT'; \$save{ 'g'}='AAGC'; \$8878 \'h' \= 'AAGG'; \$=ave('i'}-'AAGT'; \$save('j')='AATC'; \$save('k'}='AATG'; - \$eave{'l'}='AATT'; \$save{ 'm' }= 'ACAC'; \$save{ 'n' }~ 'ACAG' ; Seave { 'o' } = 'ACAT'; \$save{ 'p' }= 'ACCC' ; \$save{'q')='ACCG'; Seave{'r'}-'ACCT'; \$mave{'m'}='ACGC'; \$55.e{'e'}='ACGG'; \$mave{'u'}='ACGT'; \$save{'V'}='ACTC'; \$mave{'w'}='ACTG'; \$save{'x'}='ACTT'/ \$8ave{'y'}='AGAG'; \$pave{'z'}='AGAT'; Seave('0'}='AGCC'; \$save('1'}='AGCG'; \$eave('2'}='AGCT'; \$save{'3'}='AGGC'; \$eave{'4'}='AGGG'; 5save('5')='ACCT'; \$cave{'6'}-'AGTC'; \$eave{'7'}='AGTG'; \$save{'8'}-'AGTT'; Ssave { '9' }= 'ATRT'; \$mave{' '}='ATCC'; \$mave{ '{'}='ATCC'; \$68ve{':'}='ATCC'; \$save{':'}='ATCC'; \$64ve{'"'}-'ATEC'; \$eave{ '\' '}='ATTC'; \$66Ve{ '?'}-'ATCC'; \$eave{'!']='ATCC'; \$save{ '#'}='CCCG'; \$84ve{'\$'}='CCCT'; \$ save { ' *' }= ' CCGG' ; \$save{'&' |= 'CCGT'; \$save{ '*' } - ' CCTG'; \$save{'(')='ATCC'; \$Bave{'}'}='ATCC';

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```
$save{'_']='CGCT';
$62Ve \'-')='ATCC';
$save{'+'}='CGGT';
$save{'-'}='COTG';
$save(')'}='CGTT';
$save('{'}-'CTCT';
$save(',')*'ATCC';
$save('.')='ATCC';
$save('|')~'CTTO';
$save{ '3' }- 'CTTT';
$save{'/'}='ATCC';
$save{'\\'}-'GGTT':
$5ave{'@'}='GTGT';
$save[ *\n"] = 'ATCC';
$ Bave { '<' } " 'GTTT';
$cave('>')='GTTT';
$mave('-')='GTTT';
```

Appendix F

```
#1/usr/bin/perl
#Scan.pl : Scans blast output
#Author: Michael Krauthammer
#Copyright: c.1999, Columbia University
#Variables
#blast input/file
$input file="genebank.result";
#program output
$output_file="match.txt";
#open datastream for file which contains blast output
    open (INPUT, '/storage/psi blast/MarkIt/programs/markIt.cesult');
while ($line=<TNPUT>){
   if ($line=-/\>gi\((\d*( (.*)\,(.*)\,(.*)/)(
   $target-$4;
   $gi =$1;
   $semantic_class=$3;
    if($line==/Length = (.*)/!{
   $lengthI=$1;
    if ($Lipe--/Identities \- (\d*)\//|}
   $length actual=$1
    if ($line=-/Query: (\d*)/}{
   Gstart-Si-
#print if Subj 1, sometimes match 2 or 3 line long
    if ($line=-/Sbjct: 1 /){
   if (($length_actual/$length]) > .9){
$target, '|..., $atart, "|', $start+$length1, "| ", $semantic class, "|", $qi, "\n";
ł
```

Appendix G

```
#1/usr/bin/perl
#nucleotide_text_parser.pl
#Author: Michael Krauthammer, c.1999 Columbia University
open (INPUT, SARCV(0));
#read uncoded input text line by line (chop it)
$all='':
while ($line=<INPUT>)(
     $all=$all.$line;
open (INPUTII, '/storage/psi-blast/MarkIt/programs/markItII.result');
open (OUTPUT, '>result.txt');
ffirst part: check matches, store positions
while ($line=<INPUTII>){
($name, $start, $end, $semantic_class, $gi) = $lins = -/(.*)\\(.*)\\(.*)\\(.*)\\(.*)\\(.*)\\;<.*)</pre>
#divide by 4 (4 letter code)
 $8tart= ($8t#rt-1) /4;
 $end=($end-1)/4;
#get substring
 if ($start |= 0){
 51etters=substr($all,$start-1,$end-$start+3)."|";
 $letters = ' '.substr($all,D,Send+2}."|";
 ($letter beginning)=$letters==/(4.)/;
 $letter end=aubatr($all,$and,1);
 $letter_endII=substr{$all,$end,2};
 #ignore matches that are in the MIDDLE of sentences, allow plurals
 $lecter_beginning=-tr/[A-2]/[a-z]/;
 $letter_end=-tr/(A-Z)/(a-z)/;
 if ((|($letter beginning==/[a-t]/)| %& ((!($letter end==/(a-z)/)} ||
 ($1etter endII=-/s /))|{
 gmake sure only the first occurence is stored at this position
    if ($save($start}==''){
    $save($start)=$end.'|'.$semantic_class.'|'.$gi;
          foreach $key(keys(%save)){
    {$end key] = $pave{5key}= -/^(.*)\|/;
    if ($end_key>$end){
       if ($keyc$start){
          $save($start)='null',
    }
```

```
#second part: print out marked up document
scrt(%save);
for ($i=0:$i<length($all);$i++){
    if (()$save($i}=='null') && ($save($i}=-/./))(
    {$end,$semantic_class)=$save{$i}=-/(.*)\|(.*)\{/;
    print OUTPUT "<phr="',$semantic_class,\">';
    $store=substr($all,$i,$end-$i);
    print OUTPUT $store;
    print OUTPUT "</phr>";
    $i=$end-1;
    ) clse {
    $store=substr($all,$i,1);
    print OUTPUT $store;
}
```

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